

Db 335 CAGAACGGGCGGCTCGCGGTTGAGGTCTCGGTGCCAGTGCCTCGACGCGACGTGC 394
QY 301 TCGGCGCTGTGATCGGCGCGCGCTGAGGCGTCTTCGCTGCAACAGTCAAGACCGGTGCC 360
Db 395 TCGGCGCTGTGATCGGCGCGCGCTGAGGCGTCTTCGCTGCAACAGTCAAGACCGGTGCC 454
QY 361 GGGCGGATGATCTATCAGTTTCGGCCCTGCTCCGACGCGCGGAGGCGACGATTCGG 420
Db 455 GGGCGGATGATCTATCAGTTTCGGCCCTGCTCCGACGCGCGGAGGCGACGATTCGG 514
QY 421 CTCGGCGCTCGATCGGCGTGGGTCCGTCCGGCCGAGCACACAGCATCCACCCGAGGTGCA 480
Db 515 CTCGGCGCTCGATCGGCGTGGGTCCGTCCGGCCGAGCACACAGCATCCACCCGAGGTGCA 574
QY 481 GCAACGGGTCCCGACGCGTGCACATCTCCAGTGCATGAACGCGCGAGCTCGGGAACGT 540
Db 575 GCAACGGGTCCCGACGCGTGCACATCTCCAGTGCATGAACGCGCGAGCTCGGGAACGT 634
QY 541 CGGGCGCAGCAGCAGTGTGTTTCAGATGGCAGTCCGCGTGCATGATCCGGGTTCGGCGT 600
Db 635 CGGGCGCAGCAGCAGTGTGTTTCAGATGGCAGTCCGCGTGCATGATCCGGGTTCGGCGT 694
QY 601 CGTCCGGCTTCGCGAGTCCAGCAGTCCGGCGAGCACATGCACCCGAGCGAAGCACTCGG 660
Db 695 CGTCCGGCTTCGCGAGTCCAGCAGTCCGGCGAGCACATGCACCCGAGCGAAGCACTCGG 754
QY 661 GCGCGGATCTGATCAGCTCGGCGAGCGGGTCCCGAGCAACGCCAGCGTGGGAAGCAC 720
Db 755 GCGCGGATCTGATCAGCTCGGCGAGCGGGTCCCGAGCAACGCCAGCGTGGGAAGCAC 814
QY 721 GAGACGGCGGATGTCGCGCGCAGCAGCGCGCGCGCGCGTGCACCCGCGGAGCAGCGGC 780
Db 815 GAGACGGCGGATGTCGCGCGCAGCAGCGCGCGCGCGCGTGCACCCGCGGAGCAGCGGC 874
QY 781 CCGCGACCGCTCGGAGTGCACCCGCGCGCGCACCGCGCGCGTGGTTCAGCATCAGC 840
Db 875 CCGCGACCGCTCGGAGTGCACCCGCGCGCGCACCGCGCGCGTGGTTCAGCATCAGC 934
QY 841 CACGGGATGATCTGATCGCGAGGATCACGAACAGTAAAGCGTGTTCGGTTGAATCCA 900
Db 935 CACGGGATGATCTGATCGCGAGGATCACGAACAGTAAAGCGTGTTCGGTTGAATCCA 994
QY 901 ATGTGCTGTACGAGGATCCGATGCGGACACCGACCGAGCAGTGCATCTGTC 960
Db 995 ATGTGCTGTACGAGGATCCGATGCGGACACCGACCGAGCAGTGCATCTGTC 1054
QY 961 TCGGCACCTTCGCGGTTCACGCGCGGTGCTGGCTCCGCAACCGCGCGCGATGTCCGCGCG 1020
Db 1055 TCGGCACCTTCGCGGTTCACGCGCGGTGCTGGCTCCGCAACCGCGCGCGATGTCCGCGCG 1114
QY 1021 CCGGTGCGCGCGCTCTCCATGCGCGGTTTCGTTTCAGTTCGTCGCTGCGGTGGTTCGTC 1080
Db 1115 CCGGTGCGCGCGCTCTCCATGCGCGGTTTCGTTTCAGTTCGTCGCTGCGGTGGTTCGTC 1174
QY 1081 GAGCGGCGCGCGCGCTTCGTCGTCGATAGGGATCTATCAGCGAGTGGGCGCTC 1140
Db 1175 GAGCGGCGCGCGCGCTTCGTCGTCGATAGGGATCTATCAGCGAGTGGGCGCTC 1234
QY 1141 CAGCGGTACTTTCGCGCGCGCGCTTCGTCGTCGATAGGGATCTATCAGCGAGTGGGCGCTC 1200
Db 1235 CAGCGGTACTTTCGCGCGCGCGCTTCGTCGTCGATAGGGATCTATCAGCGAGTGGGCGCTC 1294
QY 1201 GCCAGATACACCGCGGTCGCGCGCATGTCAGATCGTGGCCAGCGCGCGCGCACCG 1260
Db 1295 GCCAGATACACCGCGGTCGCGCGCATGTCAGATCGTGGCCAGCGCGCGCGCACCG 1354
QY 1261 TGGAGATCGGATCTATCGCGCGCTGTCGGGAGGAGCGGAGGCGGTCGACT 1320
Db 1355 TGGAGATCGGATCTATCGCGCGCTGTCGGGAGGAGCGGAGGCGGTCGACT 1414
QY 1321 ACSTCGCGCGGTTGGCGAGAGCAGGACTACATCCAGCCAGCGCTTCGCGCAACATCGGGC 1380

Db 1415 ACGTCGCGCGGTTGGCGAGAGCAGGACTACATCGACCGAGCCTTGGCGAATCGGGC 1474
QY 1381 CGTATCTGCCAGCTAGGTTCCCGTCTCGTCCGATCTATCGCGCGCACCGCGCGGTGC 1440
Db 1475 CGTATCTGCCAGCTAGGTTCCCGTCTCGTCCGATCTATCGCGCGCACCGCGCGGTGC 1534
QY 1441 CCGGCACCGCGTGGATCGTTTCGTAGTACCCGAAAGCTCTTGAGAGCTAAGGCCAATTGGG 1500
Db 1535 CCGGCACCGCGTGGATCGTTTCGTAGTACCCGAAAGCTCTTGAGAGCTAAGGCCAATTGGG 1594
QY 1501 AAGATATCTGGACCTTCCCATCAATAGAGAAAGCATCGCCCTAGGGGATCCGTAGCGG 1560
Db 1595 AAGATATCTGGACCTTCCCATCAATAGAGAAAGCATCGCCCTAGGGGATCCGTAGCGG 1654
QY 1561 GCGCGGTGTTTCAGTGAACCTTGGGCGAGGCAATCCCATCGCGCGACCGCGCGAGCGG 1620
Db 1655 GCGCGGTGTTTCAGTGAACCTTGGGCGAGGCAATCCCATCGCGCGACCGCGCGAGCGG 1714
QY 1621 AAATCCACGATCCCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1655
Db 1715 AAATCCACGATCCCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1749

RESULT 2
AR201276
LOCUS AR201276 1749 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 56 from patent US 6358734.
ACCESSION AR201276
VERSION AR201276.1 GI:20252164
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1749)
AUTHORS Delcayre,A.
TITLE Compounds for treatment of infectious and immune system disorders
and methods for their use
JOURNAL Patent: US 6358734-A 56 19-MAR-2002;
FEATURES
source
1..1749
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 61.1%; Score 1011.4; DB 6; Length 1749;
Best Local Similarity 78.9%; Pred. No. 7.9e-126;
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;
QY 1 GATCTATCTACTCGACCTTTCGCGCGACCGGGCGGTACCGGGTGGCTTGAAGTACTCGGGCC 60
Db 95 GATCTATCTACTCGACCTTTCGCGCGACCGGGCGGTACCGGGTGGCTTGAAGTACTCGGGCC 154
QY 61 ATCCGCTGGCGACCGCGTTCGCGCGTGCAGACGATCAACGCGATGGAAGACGAAGGCGATGG 120
Db 155 ATCCGCTGGCGACCGCGTTCGCGCGTGCAGACGATCAACGCGATGGAAGACGAAGGCGATGG 214
QY 121 TGGCCAAACGCTCCCGCATCGCGGAGCGAGTCTCTCGGACCGGGTCTGCGCGATCTCGCGCG 180
Db 215 TGGCCAAACGCTCCCGCATCGCGGAGCGAGTCTCTCGGACCGGGTCTGCGCGATCTCGCGCG 274
QY 181 CCGCGCACCGTTTCGGTTCGGCGGAAAGTCCGCGGCTCGCGGTCTTCTGGGGGGGATCTGATC 240
Db 275 CCGCGCACCGTTTCGGTTCGGCGGAAAGTCCGCGGCTCGCGGTCTTCTGGGGGGGATCTGATC 334
QY 241 CAGAACGGGCGCGTCTCGCGGTTGAGGTCTTCGCTGCCAGTGCCTGCGCGACGCGTGC 300
Db 335 CAGAACGGGCGCGTCTCGCGGTTGAGGTCTTCGCTGCCAGTGCCTGCGCGACGCGTGC 394
QY 301 TCGGCGCTGCTGATCGGCGCGCGGTAGGCGTCTTCGCTCCACAACTGACAGCCGTCGCC 360
Db 395 TCGGCGCTGCTGATCGGCGCGCGGTAGGCGTCTTCGCTCCACAACTGACAGCCGTCGCC 454
QY 361 GGGCGGATGATCTATCAGTTTCGGCCCTGCTCCGACGCGCGGAGGCGACGATTCGG 420

Db 455 GGGCGGATGATCT---GATCGGAGGATACGAAACAGTAAGCGGTGTTCCGGTTGAA 510
Qy 421 CTCGGCGGTGATCGGGTTGGGTCCGTCCGGCCAGCACACAGCATCCACCCGAGTCCA 480
Db 511 TCCAATGTGTGTGTCAGAGGATCCGA-----TGCCGAACACCGACACGCGAGAGTC 564
Qy 481 GCAAGGGTCCCGAGCGGTGCATCTCCAGTTCGATGAACGCGCGAGTCCGGGACGT 540
Db 565 GCATCTGTCTCGGACCTTGGGTGTCAGGGGGTGTGGCTCCGAAACCGCGCGCAT 624
Qy 541 CGCGGCGAGCAGCAGTGTGTTTCAGATGGCAGTTCGCCGTGCAATGATCCCGGGTTCGGCGT 600
Db 625 GTCCGCGCGCGCT-----GGGCGCGCTCTCCATGGCCGCGTTCGTTCACT 671
Qy 601 CGTCGGGCTTCGCGGATCGAGTCAGCCAGTCAGGAGCAGATGACCGGAGGAGACGATCCG 660
Db 672 CGTCGTCCGGTGGCTGTTCTCGGAACGGGCGCGCGCGCGCTGCTCCG-----TCCG 724
Qy 661 GCGCGGATCTGATCAGTCCGGGAGCGCGGTGCCAGCAACCGCAGCGTGGGAAGCACC 720
Db 725 ATACGGGATCTGATCAGCTCGGGAGCGCGGTGCCAGCAACCGCAGCGTGGGAAGCACC 784
Qy 721 GAGACGGCGGATGTGCCCGCAGCAGCGCCAGCGGTGCAACCCCGGGGACCGGGCC 780
Db 785 GAGACGGCGGATGTGCCCGCAGCAGCGCCAGCGGTGCAACCCCGGGGACCGGGCC 844
Qy 781 CCGGAGACCGGTGCGAGTGCACCCCGCGCGCACCGCGCGCGGTGTCAGCATCAGC 840
Db 845 CCGGAGACCGGTGCGAGTGCACCCCGCGCGCACCGCGCGCGGTGTCAGCATCAGC 904
Qy 841 CAGGGATGATCT---GATCGGAGGATCAGCAACAGTAAAGCGGTGTTCCGGTTGAA 896
Db 905 CAGGGATGATCTATCAGTTCGGCCCTGTGTCGAGCCCGCGCGCGGTGTCAGTCCG 964
Qy 897 TCCAATGTGTGTCAGCAGGATCCGA-----TGCCGAACACCGACCGCAGCAGTC 950
Db 965 CTCGGGCTGATCGGGTTGGTCCGTCCGGCCAGCACACAGCATCCACCGAGTCCA 1024
Qy 951 GCAATGTGTCTGGGACCTTGGGTGTCAGCGGGGTGTCGGCTCGCAACCCCGCGGGAT 1010
Db 1025 GCAACGGGTCCCGACGTCATCTCCAGTTCGATGAACCGCGCGAGTCCGGGACGT 1084
Qy 1011 GTCCGCGCGCGCT-----GGGCGCGCTCTCCATGGCGGTGTTCTCAGT 1057
Db 1085 CGCGGCGCAGCAGCATGTTTTCAGATGGCAGTCCCGTGCATGATCCCGGGTTCGGCGT 1144
Qy 1058 CGCTCGTCCGTGCTGTTCTGGAACGGGCGCGCGCGCGCTGCTCCG-----TCCG 1110
Db 1145 GTCGGGCTTCGGGAGTCCAGCNGTTCGGGAGCAGATGACCGAGGAGCAGACTCG 1204
Qy 1111 ATACGGGATCTATCAGCAGGTAGCGGTCCAGCGGTACTCTTCGCCCCAGAACAGCGGT 1170
Db 1205 GCGCGGATCTATCAGCAGGTAGCGGTCCAGCGGTACTCTTCGCCCCAGAACAGCGGT 1264
Qy 1171 GCCTCCCGGCGAGACAGCGGTCTGCGCGCAGATACACCGGCGGTGGCGGCATG 1230
Db 1265 GCGTCCCGGCGAGACAGCGGTCTGCGCGCAGATACACCGGCGGTGGCGGCATG 1324
Qy 1231 TCCAGATGCTGGCGCAGCGCGGACCGGTGAGATCGGATCTATCGCGGCTGTGCG 1290
Db 1325 TCCAGATGCTGGCGCAGCGCGGACCGGTGAGATCGGATCTATCGCGGCTGTGCG 1384
Qy 1291 GGAAGGACGAGCGGTAGCGGCTTGCATACGTCCGCCCGGTGGCGAAGCAGGACT 1350
Db 1385 GGAAGGACGAGCGGTAGCGGCTTGCATACGTCCGCCCGGTGGCGAAGCAGGACT 1444
Qy 1351 ACATCGACGAGCGCTTGGGCAACATCGGGCGGTATCTGCCAGCTGAGGTTCCCGCTTCG 1410
Db 1445 ACATCGACGAGCGCTTGGGCAACATCGGGCGGTATCTGCCAGCTGAGGTTCCCGCTTCG 1504
Qy 1411 TCGGATCTATCGCGCAGCGCGGTGCGCGCAGCATCGGTCGTTGATGTTTCGTCAGTACC 1470

Db 1505 TCGGATCTATCCCGGACCGCGCGGTGCCCGCACCGGTGGATCGTTCGTCAGTACC 1564
Qy 1471 CGAAGCTCTTGAGAGCTAAGGCCAATTGGGAAGATATCTTGGACCTTCCCATCAATAGAGG 1530
Db 1565 CGAAGCTCTTGAGAGCTAAGGCCAATTGGGAAGATATCTTGGACCTTCCCATCAATAGAGG 1624
Qy 1531 AAAAGCATCGCCTTAGGGGATCCGTAGCGGGCCCGTGTTCGAGTGAACCTTTGGGACGG 1590
Db 1625 AAAAGCATCGCCTTAGGGGATCCGTAGCGGGCCCGTGTTCGAGTGAACCTTTGGGACGG 1684
Qy 1591 CAATCCCATCGCGCAGCCCGCGCAGCGGAAATCCACGGATCCCATCACCATCACCATC 1650
Db 1685 CAATCCCATCGCGCAGCCCGCGCAGCGGAAATCCACGGATCCCATCACCATCACCATC 1744
Qy 1651 ACTGA 1655
Db 1745 ACTGA 1749

RESULT 3
AR201277
LOCUS AR201277 1749 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 57 from patent US 6358734.
ACCESSION AR201277
VERSION AR201277.1 GI:20252165
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Delcayre,A.
TITLE Compounds for treatment of infectious and immune system disorders
and methods for their use
JOURNAL Patent: US 6358734-A 57 19-MAR-2002;
FEATURES Location/Qualifiers
source 1. .1749
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 44.7%; Score 740.2; DB 6; Length 1749;
Best Local Similarity 69.0%; Pred. No. 1.2e-89;
Matches 1244; Conservative 0; Mismatches 263; Indels 296; Gaps 5;

Qy 1 GATCTATCTACTCGACCTTTCGCGACCGCGGTACCCGGTGGCTGACGATCTCCGGCC 60
Db 95 GATCTATCTACTCGACCTTTCGCGACCGCGGTACCCGGTGGCTGACGATCTCCGGCC 154
Qy 61 ATCCGCTGGCGACCGCTTCGCGGTTCGCAACGATCAACGCGATGGAAGAGGATGG 120
Db 155 ATCCGCTGGCGACCGCTTCGCGGTTCGCAACGATCAACGCGATGGAAGAGGATGG 214
Qy 121 TGCCCAACGCTGCCCGATTCGCGGAGAGGTGCTCGACCGGGTCTGCGCGATCTCCCG 180
Db 215 TGCCCAACGCTGCCCGATTCGCGGAGAGGTGCTCGACCGGGTCTGCGCGATCTCCCG 274
Qy 181 CCGCGCACGCTTCGCTCGGGAAGTCCCGGCTTCGCGCTTCCTGCGCGGATCTGATC 240
Db 275 CCGCGCACGCTTCGCTCGGGAAGTCCCGGCTTCGCGCTTCCTGCGCGG----- 324
Qy 241 CAGAACGGGCGGCTCTCGGGTTGAGGTCTCTCGGTGCCAGTGCCTGCGACGCGACGTG 300
Db 325 ----- 324
Qy 301 TCGGCGCTGTGTATGCGGCGCGCGTGGCTCCTCGGTCCACAACTCAGCAGCGTCCCG 360
Db 325 ----- 324
Qy 361 GGGCGGATGATCTATCAGTTCGGCCCTGCTGCCAGCCCGCGGAGGCGAGCAGTTCCG 420
Db 325 -----GGCTATCAGTTCGGCCCTGCTGCCAGCCCGCGGAGGCGAGCAGTTCCG 376
Qy 421 CTCGGGCTGATCGGGTTGGGTCCGTCGCGCGCAGCACACAGCATCCACCGAGGTGCA 480

Db 377 CTCGCGCGTCGATCGGGTTGGTTCGTCGCGCAGCAGCATCCACCCGAGGTGCA 436
QY 481 GCAACGGGTCCCAGCGGTGCAATCTCCAGTTCGATGAACCCCGAGCTCGGGAGCT 540
Db 437 GCAACGGGTCCCAGCGGTGCAATCTCCAGTTCGATGAACCCCGAGCTCGGGAGCT 496
QY 541 CGGCGCGCAGCAGCAGTGTTCAGATGCGCAGTTCGCGGTGCAATGATCCGGGTTCGGGT 600
Db 497 CGGCGCGCAGCAGCAGTGTTCAGATGCGCAGTTCGCGGTGCAATGATCCGGGTTCGGGT 556
QY 601 CGTCCGGCTCGCGCAGTCCAGCAGTTCGCGCAGCAGCAGTCCAGCAGGGAACGACTCGG 660
Db 557 CGTCCGGCTCGCGCAGTCCAGCAGTTCGCGCAGCAGCAGTCCAGCAGGGAACGACTCGG 616
QY 661 GCGCGGATCTGATCAGTTCGCGGAGCCGCGGTGCCAGCAACCCAGCAGTGGGAAGCACC 720
Db 617 GCGCGGATCTGATC-----GGCAGGATCAGCAACAGTAAGCGGTGTCGGGT 666
QY 721 GAGACGGCGCATGTGCGCGCAGCAGCGGCCAGCGTGCACCCCGCGGAGCCGGCC 780
Db 667 GAATCCAATGTGTCGACGAGCATCCGATGCCGAACACCAGCACCGGAGCAGTCGCA 726
QY 781 CGCGGACCGGTGCGAGTTCGACCCCGCGCGCCACCGCGCGCGTGTGTCAGCATCAGC 840
Db 727 ATCTGTCTCGGACCTCGGGTTCAGCGGGTGTGCTCCGGAACCCCGCGCATGTC 786
QY 841 CACGGGATGATCTGATCGCGAGGC---ATCAGAACAGTAAGCGGTGTCGGTGAAT 897
Db 787 GCGCGCGCGTTCGCGCGCGCTCTCCATGCGCGGTTCGTTAGTCGTCGTCGGTGGCT 846
QY 898 CCNATGTGTGTCAGCAGGATCCGATGCGGAACACCGGACCGGAGCAGTCGCNATCT 957
Db 847 GTTCTCGAACCGGCGCGCGCGCTGTCGTCGATACCGGATCTGATCAGTCGCG 906
QY 958 GTCTCGCGACCTTGGGTTCAGCGCGGTCTGTGCTCCGCAACCCCGCGCGATGTCGCG 1017
Db 907 GAGCGGGTCCAGCAACCGCAGTGGGAACACCGGAGCAGCGGCGCATGTGCCGCG 966
QY 1018 GCGCGCTCGCGCGCGCTCTCCATGCGCGGTTCGTTAGTCGTCGTCGCGGTGCTGTC 1077
Db 967 CAGCAGCGCGCAGCGTGCACCCCGCGGAGCCGCGCGCGCGCGCGTTCGAGTCGAC 1026
QY 1078 TCGGAACGGCGCGCGCGCGC-----CGTCTGTCGTCGATACGGGATCTACGCGAG 1130
Db 1027 CCGCGCGCGCACCGCGCGCGCGTGTGTCAGCATCAGCCACGGGATGATCTATCAGCAG 1086
QY 1131 GTAGGCGGTCCAGCGGTACTTTCGCGCCAGAACAGCGGTGCGTCCGCGCGCAGACCA 1190
Db 1087 GTAGGCGGTCCAGCGGTACTTTCGCGCCAGAACAGCGGTGCGTCCGCGCGCAGACCA 1146
QY 1191 CGGTCTGCGCGCAGATACACCCAGCGGTGCGCGGATGTTCAGATCGTGGCAGCGCG 1250
Db 1147 CGGTCTGCGCGCAGATACACCCAGCGGTGCGCGGATGTTCAGATCGTGGCAGCGCG 1206
QY 1251 CGCGGACCGGTGAGATCGGATCTATCGCGCGCTGTGCGGGAAGCAGCGCGGTAGCG 1310
Db 1207 CGCGGACCGGTGAGATCGGATCTATCGCGCGCTGTGCGGGAAGCAGCGCGGTAGCG 1266
QY 1311 CGGTCTGACATACGTTCGCGCGCGGTGCGGAAGCAGGACTACATCGACCGAGCTTTCGCG 1370
Db 1267 CGGTCTGACATACGTTCGCGCGCGGTGCGGAAGCAGGACTACATCGACCGAGCTTTCGCG 1326
QY 1371 AACATCGGCGCGTATCTGCGCAGCTGAGGTTCCCGCTCTCGTCTCG----- 1413
Db 1327 AACATCGGCGCGTATCTGCGCAGCTGAGGTTCCCGCTCTCGTCTCGGATCTGATCAGAACCG 1386
QY 1414 ----- 1413
Db 1387 GCGCGTCTCGGGTTGAGTCTCTCGGTGCGCAGTGCAGCGCGGTTCGCGCGGT 1446
QY 1414 ----- 1413

Db 1447 GGTATGCGCGCGCGTAGGCGTCTCTGGTCCACAAAGTCAGCAGCCGTGCCGCGCGAT 1506
QY 1414 -GATCTATCGCGCGCACCGCGCGGTGCGCGCAGCGCGTGGATCGTTCTGTCAGTACCG 1472
Db 1507 GGTATCTATCGCGCGCACCGCGCGGTGCGCGCAGCGCGTGGATCGTTCTGTCAGTACCG 1566
QY 1473 AAGCTCTTTGAGAGCTTAAGGCCAAATTGGGAAGATACTTTGGACCTTCCCATCAATAGAGAA 1532
Db 1567 AAGCTCTTTGAGAGCTTAAGGCCAAATTGGGAAGATACTTTGGACCTTCCCATCAATAGAGAA 1626
QY 1533 AAGCATCCCTTAGGGATCCGTAGCGCGCGCGGTGTTTTCAGTGAATCTTGGCGAGGCA 1592
Db 1627 AAGCATCCCTTAGGGATCCGTAGCGCGCGCGGTGTTTTCAGTGAATCTTGGCGAGGCA 1686
QY 1593 ATCCCATCGCGCAGCGCGCGGAGCAATCCACCGATCCCATCACCATCACCATCAC 1652
Db 1687 ATCCCATCGCGCAGCGCGCGGAGCAATCCACCGATCCCATCACCATCACCATCAC 1746
QY 1653 TGA 1655
Db 1747 TGA 1749

RESULT 4
AR201235
LOCUS AR201235 291 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 15 from patent US 6358734.
ACCESSION AR201235
VERSION AR201235.1 GI:20252123
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 291)
AUTHORS Delcayre, A.
TITLE Compounds for treatment of infectious and immune system disorders
and methods for their use
JOURNAL Patent: US 6358734-A 15 19-MAR-2002;
FEATURES Location/Qualifiers
source 1..291
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 17.6%; Score 291; DB 6; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.5e-29; Mismatches 0; Indels 0; Gaps 0;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 375 ATCAGTTCGGCCCTGCTGCGCCAGCCCGCGGAGGCGAGGTCGCGTCCGCGTCGATC 434
Db 1 ATCAGTTCGGCCCTGCTGCGCCAGCCCGCGGAGGCGAGGTCGCGTCCGCGTCGATC 60
QY 435 GGGTTGGGTTCGTCGCGCCAGCACACCGATCCACCGAGGTCCAGACACGGGTCCCG 494
Db 61 GGGTTGGGTTCGTCGCGCCAGCACACCGATCCACCGAGGTCCAGACACGGGTCCCG 120
QY 495 ACGGTGCAATCTCCAGTTCGATGAACCGCGAGCTCGGGAGCTCGCGCGCAGCAGC 554
Db 121 ACGGTGCAATCTCCAGTTCGATGAACCGCGAGCTCGGGAGCTCGCGCGCAGCAGC 180
QY 555 ACGTTGTTTCAGATGCGCAGTTCGCGGTGATGATCCCGGTTCGCGGTTCGCGGTTCGCG 614
Db 181 ACGTTGTTTCAGATGCGCAGTTCGCGGTGATGATCCCGGTTCGCGGTTCGCGGTTCGCG 240
QY 615 GAGTCCAGCAGTCCGCGAGCAGTCCACCGAGCGGAGCAGTCCGGGCGC 665
Db 241 GAGTCCAGCAGTCCGCGAGCAGTCCACCGAGCGGAGCAGTCCGGGCGC 291

RESULT 5
AR201238
LOCUS AR201238 261 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 18 from patent US 6358734.


```
Query Match      10.7%; Score 177; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 672 GATCAGCTGGGAGCGCGGTGCCAGCAACGCGTGGGAGCAGCAGCAGCAGCGGCGC 731
Db 1 GATCAGCTGGGAGCGCGGTGCCAGCAACGCGTGGGAGCAGCAGCAGCAGCGGCGC 60

QY 732 GATGTCGCCGCGCAGCAGCGCCAGCGTGCACCCCGCGGAGCCCGGCCCGCGGACCGC 791
Db 61 GATGTCGCCGCGCAGCAGCGCCAGCGTGCACCCCGCGGAGCCCGGCCCGCGGACCGC 120

QY 792 GTCGAGTGCACCCCGCGCGCACCGCGCGCGCGTGCAGTCAGCAGCAGCGGAT 848
Db 121 GTCGAGTGCACCCCGCGCGCACCGCGCGCGCGTGCAGTCAGCAGCAGCGGAT 177

RESULT 9
AR201236
LOCUS      147 bp      DNA      linear      PAT 20-APR-2002
DEFINITION      Sequence 16 from patent US 6358734.
ACCESSION      AR201236
VERSION      AR201236.1 GI:20252124
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 147)
AUTHORS      Delcayre,A.
TITLE      Compounds for treatment of infectious and immune system disorders
JOURNAL      Patent: US 6358734-A 16 19-MAR-2002;
FEATURES      Location/Qualifiers
source      1. .147
/mol_type="unassigned DNA"

ORIGIN
Query Match      8.9%; Score 147; DB 6; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1122 ATACGAGTAGGCGTCCAGCGCTACTCTTCGCCCCAGAACAGCGGTGCCGTGCCCGC 1181
Db 1 ATACGAGTAGGCGTCCAGCGCTACTCTTCGCCCCAGAACAGCGGTGCCGTGCCCGC 60

QY 1182 GCAGCAGCGGTCTCTCCGCCAGATACACCCAGCGGTGCCCGCATGTCCAGATCGTG 1241
Db 61 GCAGCAGCGGTCTCTCCGCCAGATACACCCAGCGGTGCCCGCATGTCCAGATCGTG 120

QY 1242 GCCAGCGCGCGCACGCTGGAGATC 1268
Db 121 GCCAGCGCGCGCACGCTGGAGATC 147

RESULT 10
AR201237
LOCUS      138 bp      DNA      linear      PAT 20-APR-2002
DEFINITION      Sequence 17 from patent US 6358734.
ACCESSION      AR201237
VERSION      AR201237.1 GI:20252125
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 138)
AUTHORS      Delcayre,A.
TITLE      Compounds for treatment of infectious and immune system disorders
JOURNAL      Patent: US 6358734-A 17 19-MAR-2002;
FEATURES      Location/Qualifiers
source      1. .138
/mol_type="unassigned DNA"

ORIGIN
Query Match      8.3%; Score 138; DB 6; Length 138;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 ATCCGCGCGCTGCGGGAAGAGAGCGCGTAGCGGCTTGCACTACGTGCGCCCGGTT 1334
Db 1 ATCCGCGCGCTGCGGGAAGAGAGCGCGTAGCGGCTTGCACTACGTGCGCCCGGTT 60

QY 1335 GCGCAGAGCAGGAGCTACATCAGCAGCGCTTGGCAACATCGGCGCGTATCTGCCAGCT 1394
Db 61 GCGCAGAGCAGGAGCTACATCAGCAGCGCTTGGCAACATCGGCGCGTATCTGCCAGCT 120

QY 1395 GAGGTTCGCGCTCTCGTC 1412
Db 121 GAGGTTCGCGCTCTCGTC 138

RESULT 11
AP005039/c
LOCUS      29925 bp      DNA      linear      BCT 10-MAY-2003
DEFINITION      Streptomyces avermitilis genomic DNA, complete genome, section 19/30.
ACCESSION      AP005039 BA000030
VERSION      AP005039.1 GI:29608072
KEYWORDS      .
ORGANISM      Streptomyces avermitilis MA-4680
SOURCE      Streptomyces avermitilis MA-4680
REFERENCE      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
AUTHORS      Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C., Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osone,T., Kikuchi,H., Shiba,T., Sakaki,Y. and Hattori,M.
TITLE      Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
MEDLINE      21477403
PUBMED      11572948
AUTHORS      Ikeda,H., Ishikawa,J., Hanamoto,A., Shinose,M., Kikuchi,H., Shiba,T., Sakaki,Y., Hattori,M. and Omura,S.
TITLE      Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
JOURNAL      Nat. Biotechnol. 21 (5), 526-531 (2003)
MEDLINE      22608306
PUBMED      12692562
AUTHORS      Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C., Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osone,T., Kishida,N., Director-General of Biotechnology Center, Shiba,T., Sakaki,Y. and Hattori,M.
TITLE      Direct Submission
JOURNAL      Submitted (29-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nitech.go.jp, URL:http://www.bio.nitech.go.jp/, Tel:81-3-3481-1933, Fax:81-3-3481-8424)
COMMENT      This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osone(*4), Norihiro Kishida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7) and Satoshi Omura(*1,*3).
Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.
*1 Kitasato Institute for Life Sciences, Kitasato University
*2 National Institute of Infectious Diseases
*3 The Kitasato Institute
```

*4 National Institute of Technology and Evaluation
*5 School of Science, Kitasato University
*6 Institute of Medical Science, University of Tokyo
*7 RIKEN, Genomic Sciences Center
Following url is also available.
<http://avermitilis.lis.kitasato-u.ac.jp>.

FEATURES
source

1. 299925
/organism="Streptomyces avermitilis MA-4680"
/mol_type="genomic DNA"
/strain="MA-4680"
/db_xref="taxon:227882"
/notes="This strain is also named as strain: ATCC 31267,
NCIMB 12804 or NRRL 8165.--synonym: Streptomyces
avermiticinus"

CDS

39. .788
/note="SAV4416"
/codon_start=1
/transl_table=11
/product="putative two-component system response
regulator"
/protein_id="BAC72128.1"
/db_xref="GI:29608073"
/translation="MOOPYEFGAEAVERGAGAGARLVVDDDPTRPVAVVSGYLDRAG
YVVDRAEDGTALARAAMPDVLVLDLMLPGMDGLEVCRRMRGPGVPVIMLTARGD
EDRIILGLEVDADYTKPSRELVLVESVLRTPTAPPLHSLGLADPAARR
ATKDGELATITREFDLIAFFLRHGRFASREDLMREVMGWDFGLDSTVTVHVRRLRG
KVDDPAPRLIQTIVMGVYRFGTTTPEQAV"

CDS

791. .1915
/note="SAV4417"
/codon_start=1
/transl_table=11
/product="putative two-component system sensor kinase"
/protein_id="BAC72129.1"
/db_xref="GI:29608074"
/translation="MHDMLLIALFALGAAAGLCGVLVLRRLSLTVSLAVSVA
AVTMAGTLAVAMWFLSAHDTIVTVTVVMAAVSLATALLGRWVARSRELALA
ARFSGDGPAAADGPATAEILDALARELAATSARLAESDRERALSREKLVAMLSH
DLRTPLAGLMEALADGADPDRLQRTIETVERKNDVMGDLELSRIHAGTLAL
SPSRISLYDLGADAGFLARELVLDVDRVPPVPEVDGKEMSRVIGNLLIAL
RRTPADGTAAIAAERSGGVLSVTGCGGIPEDLPVFEVDTGWRGTARTPPAGAGL
GLAIVGIVEAHQQAQAVRNIPGCRFEVTLPTARAQPP"

CDS

1998. 3140
/note="SAV4418"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAC72130.1"
/db_xref="GI:29608075"
/translation="MFGTVLLLAASPAGKGLVDAAASVLPVLAAPSVLSGTDANV
VELADPLEQAVLTRRAAATAFGPLTVLAGLQQLDRORHLEPHILALARTTPSTVRYT
GFPMWTRIELRLPPGTTTLFVDLHADAEHQHRTGPLDGRAALYGRVAPPPR
RTVAPPAYMKAVATILSRGHPPEVLHEQALGRVHEGGHADI VLTTPGCGAALFEG
FVCPGAPVPPQPRPTPDGPAADVHATIAAARAGRHGADALAAQEQTAASHTGA
ASPEALHWRERADLAFMGDAARSCEAMLTAVGTRLAAGCAPADPAVEAAVRAHHQ
WGRIDDPARARELGPALADRLRVPGRREGALDHVQHLRLQLTQG"
complement (3180. .5276)
/note="SAV4419
similar to cell wall surface anchor family protein"

CDS

39. .788
/note="SAV4416"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAC72131.1"
/db_xref="GI:29608076"
/translation="MKDOLMRGHDHLLHTRADGPPYLFRAWGFEIIVIRITPLTATAL
AVLPSAALAVGSAAPALASSTLLPVRSTGDVVVDGVRHVFISDPAGKVAWATYA
GTVLGTVDLSLPGAGLELSADSGTYLAAPGADAI VADTATATEARYPTGAGTPE
YPALAGKIMFPGVGGSEGNIGSLDLSGADPVTIKDTRTWDAIILSGAGAPT
LVAGAPGQPVGLVDVSSGATLTAFADPVTGKGNLSDLATPDGKDVVTASGA
ROYQVTKISDLSADGRYQNTYPAVDIAPDGTVAAGTFSWYDPPDVHVPKGVSTEV
PYQVLTPTSSGADTLTAGSLAWSPDGSRLLFAVYNDKDVYSLRVDPDPTKAATSLT
MVAEPKTRGKALSVSGTLTSAEALPAGATVSVTRTDMESPSGKPGVGTATVAADGSYT
FGDTPPAGKRYTATTAGDASHSGATATGSVEVRSPTPILTLNNDKGVAYGSDVKF

CDS

complement (5354. .5509)
/note="SAV4420"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAC72132.1"
/db_xref="GI:29608077"
/translation="MFRRTAARYSRSAANAATAAALVAANAAGPAPAAATPPAHEASH
SRLAAPT"

CDS

5664. .7007
/note="SAV4421"
/codon_start=1
/transl_table=11
/product="putative regulatory protein"
/protein_id="BAC72133.1"
/db_xref="GI:29608078"
/translation="MADRDEPIIIGRRVORLAERGLTORQLAEPAATPAYISTLEBAG
RVASEPALRHIAIDRLGVAVELATGRPAHLATLRLTDAORTLATCEAAEASQY
AALLAEAVHGLAEAEAAALLGECATEAGDILVGRRRFEAEQRLGDAPLRVP
IRGRAVSHYLAGEIRYAVYLLESTLDELNRITGLDHPDALLLIYASVYGMQALHAR
AAQAEAFALALAPQVGDPAVMHRSVARTMLAEGRAAEADASLVKAELADVLHRRG
TELANCWNRGYLHAQNGELERAEGLERQAHSMLAQRAALYSQAAVELADVLHRRG
KSDAAALLHLVGLDLSPERGAVHSAGAHRLIGIJAEDAHDTAEAEHVVRLSLLER
AQAAGDLADLCMLGDLLRSRGRVEALDAYRTGLGHRTAGCTTTLGPAPAQPPL"
complement (7322. .7543)
/note="SAV4422"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAC72134.1"
/db_xref="GI:29608079"
/translation="MTKPSAPRRHLPTSPFAAPVAPAEKHFGLGDRVSHDQFGLGTIV
GYEGTAMLVDFGSSQARILTYTRMHSL"

CDS

complement (7614. .9236)
/gene="pbb7"
complement (7614. .9236)
/genes="pbb7"
/note="SAV4423"
/codon_start=1
/transl_table=11
/product="putative penicillin-binding protein"
/protein_id="BAC72135.1"
/db_xref="GI:29608080"
/translation="MSAPEEQRRRRI PRVTRRRRRRWRIRRALAALIMLCGA
VVAYLLTGVPHPETVTSQSTVFLDADGEYLGRRGPDVDRQDVLSEVPRHQDAVIA
AENRSPRTSGISPSAVRAAVSTLGGARQGSTITQYVKNALLSPEQSLSRKARE
ALIAVKLDTRSKDSILEGVNTVYFGRGAAGIESAARNYFGVDAKDLTLAQGAALAA
IINLPSYERAGADAKVTATLEKNSWLDGWRTSCTITAKERLAAAFPAFRVPCGN
TGRLQYLLDAATEADRLGTLQDLARGGTVTRTFDLAAQATAEQVRGAPARK
GTRHTVVALVPGDGAIVLGGADYQPFNDVNGAVEAGTALDPPKRAVFTGPL
ALMLRTAASPLRLASAAATVAGGTAKPTVTKITRGRTSTYATRPDPTRRVASVQ
AOMLTXYTGAAGAVGHFGSGGPGARTLWOTTSGRLSVTVLFAEYPAAGKRPAR
PAHLPTAPVLAAGLTSVSSKTLVEVPAGLP"
complement (9233. .9907)
/note="SAV4424"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="BAC72136.1"
/db_xref="GI:29608081"

gene

CDS

complement (9904. .10341)
/genes="sig38"
complement (9904. .10341)
/gene="sig38"

CDS

complement (9904. .10341)
/genes="sig38"
complement (9904. .10341)
/gene="sig38"

gene

CDS

complement (9904. .10341)
/genes="sig38"


```

DDVETATVDVRPYGGGDEWVVVDLGCAGVGAGGIGNHAEVGVGVGGASTTLAAGL
TVTPVSAALDLGTSGIQALHAAAHATVTA'DVNPRAHLTALTLALSGAPAADLR
EGSLIFVADDETDLIVSNPPFVIFPGALRTYDGGMGDDLLCRSLVQOTGERLNEG
GFAHLANQWHEBWTDRLSRWPHGCDAMIVQREVQDVQIYAEMLNDRDAGDRHGD
PADYQARYDLWDFEARKVAVFGWITLRTGAADPSVAEENPHVPEQLGETVR
AHPDRVYLRSHDDALLAEHAFPTLSGEVVOEQLPGCAEDPEHVILRQNRGMRATRV
DTVAGCGVCDCTMSAGRTLDAIAQLVGEDPVALRDRTPAQIRLLVEQGFLEPA"
complement(1417..1437)
/genes="SCO3545"
/notes="PS00092 N-6 Adenine-specific DNA methylases
signature."
complement(2227..2817)
/genes="SCO3546"
/notes="synonym: SCH5_09c"
complement(2227..2817)
/genes="SCO3546"
/notes="SCH5_09c, possible small lipoprotein, len: 196aa;
Contains PS00013 Prokaryotic membrane lipoprotein lipid
attachment site and probable N-terminal signal sequence.
Contains probable coiled-coil from 104 to 141 (38
residues), max score: 1.630, (probability 1.00)."
/codon_start=1
/transl_table=11
/product="putative small secreted protein"
/protein_id="CAB38483.1"
/db_xref="GI:4539564"
/db_xref="UniProt/TREMBL:Q9X912"
/transl_table=11
/translation="MEGTNPVKKLAALSGGAVLVALTGCSSSDNEKLDWSAKDV
CEGVQKQKIAEANAIOKETSDNSTPAEVKTDKAFQDMSDAYKAMGATVQKAGP
PDVDGSKQKDAVTELNGLSVASYASLRKQVEBLTDKQAKFADGLKDLATLNLKSK
SGSNALTKLREGDVGQAWAKQPSKSAVSPTSAEG"
complement(2734..2766)
/genes="SCO3546"
/notes="PS00013 Prokaryotic membrane lipoprotein lipid
attachment site."
complement(3037..5421)
/genes="SCO3547"
/notes="synonym: SCH5_10c"
complement(3037..5421)
/genes="SCO3547"
/notes="SCH5_10c, probable pyrophosphate synthase len: 794
aa; similar to many e.g. TR:O68460 (EMBL:AF044912) H+
translocating pyrophosphate synthase from Rhodospirillum
rubrum (660 aa) fasta scores; opt: 1169, z-score: 1286.1,
E(): 0, (44.6% identity in 697 aa overlap). DNA sequence
contains 35 base inverted repeat with 37 base loop
(15201..15308)."
/codon_start=1
/transl_table=11
/product="putative pyrophosphate synthase"
/protein_id="CAB38484.1"
/db_xref="GI:4539565"
/db_xref="GOA:Q9X913"
/db_xref="UniProt/TREMBL:Q9X913"
/translation="MAELPTSHLAAVLTDGNRALVAVIAVVALAALVAGLVROVL
AAGSTGSMKIAAAGVAGANAYLARQLRLGVLPAVVPFLLMLLPADNRQAGRI
FFLLGAFSAATYIGMVLAVNRVRAAREATPAPGPEKDLALVSHKATAPFR
TGGVYGTLLTGALACCCVLYAADAPKVLGEGFGLGAALIAMFMRVGGIPTKAD
VGADLVKEQGIPEDDPRNAATADNVGNVDCAGMAADLFESAVTLVAALILGK
VAFGDFGLPFLVPAIGLVTAMIGIFAVAPRRSDRSGMAINRPFISAVISLVLA
VAVVYLPKYADDDGVDTAIACKSGDPRILALVAVALGIVLVAALIQLTGTVFET
RRPYDILKSLTGTGATVVLVAGISIGLESAYVTALLGLGVYAGFLGGTSLMALFA
VALAGTLLTVGVIVAMDTPGVDNAQGAEMSGDVGAGAVLTDLDKAVGNITKA
ITKGATATATAAALFSGYDAITTTGAADVDEKLSGEGAPMTLMMDI SOPNNVLG
IAGAAVFLFGLAINAVSRGAVVVEVRQFRPGIMDYSEKPYGVKVDICTDR
ALRELATPGLIAPVAPIFIGFTLVGALGAFAGIAGITLMAVFLANSVGSWNAKK
LVEGHGKGSEHAATVIGDTPKDTAGTAIINPLKVMNLVALLIAPVIFES
YGAOKSVVVRVLIIVAFVAVIAAVYVSKRGIAIGEDDADPEPKSADPAVVS"
4668..4775
/notes="35 base inverted repeat with possible 37 base
loop."
repeat_region
5559..5564
misc_feature
/notes="Cleavage site for AseI restriction endonuclease"

```

```

AT*TAAT."
complement(5559..5564)
/notes="Cleavage site for AseI restriction endonuclease
AT*TAAT."
complement(5760..6191)
/genes="SCO3548"
/notes="synonym: SCH5_11c"
complement(5760..6191)
/genes="SCO3548"
/notes="SCH5_11c, probable anti-sigma factor, len: 143 aa;
similar to many e.g. SW:RSBW_BACSU RsbW, anti-sigma B
factor from Bacillus subtilis (160 aa) fasta scores; opt:
153, z-score: 198.9, E(): 0.00089, (28.7% identity in 136
aa overlap) and SW:SP22_BACSU SpoIIAB, anti-sigma F
factor, sporulation protein, from Bacillus subtilis (146
aa) fasta scores; opt: 125, z-score: 165.8, E(): 0.063,
(29.2% identity in 137 aa overlap)."
/codon_start=1
/transl_table=11
/product="putative anti-sigma factor"
/protein_id="CAB38485.1"
/db_xref="GI:4539566"
/db_xref="UniProt/TREMBL:Q9X914"
/translation="MATVELRFSALPEHVRTARLVAARVARRAGVDEAVLDVRLVAVG
EACTRAVGLHQHVGITAPVKVLSLIEEKQFSIEVGDEAPHAVPGVKTSGDAVDELEAE
EDBMGLAVISGLVDVEVSAGEDGGLIRMTPTASAVLPPI"
complement(6301..6642)
/genes="SCO3549"
/notes="synonyms: bldG, SCH5_12c"
complement(6301..6642)
/genes="SCO3549"
/notes="SCH5_12c, bldG, probable anti-sigma factor
antagonist, len: 113 aa; similar to many e.g.
SW:RSBW_BACSU RsbV, anti-sigma B factor antagonist from
Bacillus subtilis (109 aa) fasta scores; opt: 255,
z-score: 341.7, E(): 9.9e-12, (45.7% identity in 94 aa
overlap) and SW:SP21_BACSU spoIIAA, anti-sigma F factor
antagonist (116 aa) fasta scores; opt: 179, z-score:
244.8, E(): 2.5e-06, (30.2% identity in 96 aa overlap)."
/codon_start=1
/transl_table=11
/product="putative anti-sigma factor antagonist"
/protein_id="CAB38486.1"
/db_xref="GI:4539567"
/db_xref="UniProt/Swiss-Prot:Q9WVX8"
/translation="MDLSLSTRVGVDRVTVEVGEIDVVTAPKLREQLVLDVNDGSPH
LVVDMEGVDFLDSTGLGVLVGLKRVRAHGSRLVLCNQERILKIFRITGLTKVFPPIH
TSVEEAAVAAATD"
6752..9199
/genes="SCO3550"
/notes="synonym: SCH5_13"
Query Match 7.6%; Score 126.6; DB 1; Length 309050;
Best Local Similarity 66.2%; Pred. No. 3.3e-08;
Matches 198; Conservative 0; Mismatches 99; Indels 2; Gaps 1;
Qy 6 ATCTACTCGACCTTCGCGGACCGCGGTACCCGGTGCCTCGCTACTTCGGCCATCCG 65
|||||
84606 ATCGCCGCGACCTTCGCGGAGCGCCCTACCCGGCGGACTGACGTACTTCGGGCACCCG 84665
|||||
Qy 66 CTGCGGACCGCTTCGCGGTTCGCGACCGATCAACGCGATGGAAGACGAAGGCATGGTGCC 125
|||||
84666 CTGGCTTCGCGCGCGCGCGCTCGCCACGATCAACGTGATGCGGAGGAGGCGTCTGCGAG 84725
|||||
Qy 126 AACGCTCCCGCATTCGCGGAGCGAGGTCTCTCGACCGGGTCTGCGCGATCTCGCCGCCCGG 185
|||||
84726 CACGCGCGCGACTTCGCGCGCGAGGTCTCTCGAGCGCGCGTTCGCGGAGCTGGCCGAGCGC 84785
|||||
Qy 186 CACCGTTCGTCGCGGAAGTCCGCGGCTCTCGGCGTCTTCTGGCG--GGATCTGATCCAG 243
|||||
84786 CACCCGAGCGTGGGCGGAGGTGCGCGGACCGGCATGTTCTGGGCGCTGGAGCTGGTGGCG 84845
|||||
Qy 244 AACGGCGCGGTCTCGCGGTTGAGGTCTCTCGGTGCCAGTGCCTCGACGCGACGTCGTC 302
|||||

```

Db 84846 AACCGGAGACCGGAGCGCTGGTGCCGTACACCGACCGGGGAGCGGCCACGCC 84904

RESULT 14
AR201231
LOCUS AR201231 114 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 11 from patent US 6358734.
ACCESSION AR201231
VERSION AR201231.1 GI:20252119
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 114)
AUTHORS Delcayre,A.
TITLE Compounds for treatment of infectious and immune system disorders
and methods for their use
JOURNAL Patent: US 6358734-A 11 19-MAR-2002;
FEATURES Location/Qualifiers
1..114
source /organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 6.9%; Score 114; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1122 ATCACGAGTAGGCGTCCAGCGGTACTTTCGCCCCAGAACAGCGGTGCGGTCCGCCG 1181
Db 1 ATCACGAGTAGGCGTCCAGCGGTACTTTCGCCCCAGAACAGCGGTGCGGTCCGCCG 60

QY 1182 GCAGACACGCGTCTTCGCCCCAGATACACCCAGGCGGTGGCGGATGTCCAG 1235
Db 61 GCAGACACGCGTCTTCGCCCCAGATACACCCAGGCGGTGGCGGATGTCCAG 114

RESULT 15
AP006618_17/c
WPCOMMENT
Sequence split into 61 fragments LOCUS AP006618 Accession AP006618
Fragment Name Begin End
AP006618_00 1 110000
AP006618_01 100001 210000
AP006618_02 200001 310000
AP006618_03 300001 410000
AP006618_04 400001 510000
AP006618_05 500001 610000
AP006618_06 600001 710000
AP006618_07 700001 810000
AP006618_08 800001 910000
AP006618_09 900001 1010000
AP006618_10 1000001 1110000
AP006618_11 1100001 1210000
AP006618_12 1200001 1310000
AP006618_13 1300001 1410000
AP006618_14 1400001 1510000
AP006618_15 1500001 1610000
AP006618_16 1600001 1710000
AP006618_17 1700001 1810000
AP006618_18 1800001 1910000
AP006618_19 1900001 2010000
AP006618_20 2000001 2110000
AP006618_21 2100001 2210000
AP006618_22 2200001 2310000
AP006618_23 2300001 2410000
AP006618_24 2400001 2510000
AP006618_25 2500001 2610000
AP006618_26 2600001 2710000
AP006618_27 2700001 2810000
AP006618_28 2800001 2910000
AP006618_29 2900001 3010000

AP006618_30 3000001 3110000
AP006618_31 3100001 3210000
AP006618_32 3200001 3310000
AP006618_33 3300001 3410000
AP006618_34 3400001 3510000
AP006618_35 3500001 3610000
AP006618_36 3600001 3710000
AP006618_37 3700001 3810000
AP006618_38 3800001 3910000
AP006618_39 3900001 4010000
AP006618_40 4000001 4110000
AP006618_41 4100001 4210000
AP006618_42 4200001 4310000
AP006618_43 4300001 4410000
AP006618_44 4400001 4510000
AP006618_45 4500001 4610000
AP006618_46 4600001 4710000
AP006618_47 4700001 4810000
AP006618_48 4800001 4910000
AP006618_49 4900001 5010000
AP006618_50 5000001 5110000
AP006618_51 5100001 5210000
AP006618_52 5200001 5310000
AP006618_53 5300001 5410000
AP006618_54 5400001 5510000
AP006618_55 5500001 5610000
AP006618_56 5600001 5710000
AP006618_57 5700001 5810000
AP006618_58 5800001 5910000
AP006618_59 5900001 6010000
AP006618_60 6000001 6021225
Continuation (18 of 61) of AP006618 from base 1700001 (AP006618 Nocardia farcinica IFM 1)

Query Match 6.2%; Score 102.4; DB 1; Length 110000;
Best Local Similarity 54.6%; Pred. No. 6.7e-05;
Matches 248; Conservative 0; Mismatches 201; Indels 5; Gaps 2;
QY 362 GCGCGATGGATCTATCAGTTGGCCCTGTGTCGCCAGCGCGCGGAGTCCGAGTTCGCCG 421
Db 55118 GCCGTAGTGTCTGACCATCTCTCGGAGTGGGAGGCCACCGGTGCAACCGAGCGTGC 55059

QY 422 TCCGGCGTGTGATCGGGTTGGGTCG---TCCGGCCAGCACACACGATCCACCCGAGGTC 478
Db 55058 GACCAGCGCGCGCGCGTGTCCCGGCTCCCGGGGTCCGGGTGCGGATCTGCGAGCCAGATC 54999

QY 479 GAGCAACGGGTCCCGACGGTGCATCTCCAGTCGATGACGCGCGGAGCTCCGGGAC 538
Db 54998 CAGCAGCGGGTCCCGATGGTGGACATCTCCAGTCGACACGCGCGGACCTGCGGACC 54939

QY 539 GTCGCGGCGCAGCAGCACGCTTGTTCAGATGGCAGTCGCGGTGCATGATCCCGGTTTCGGC 598
Db 54938 GTCGTAGGAGAACATGATGTTGGCCAGTGGCAGTGGCAGTCCGCGTCCAGAGTCCCGGGTCCA 54879

QY 599 GTCGTGCGGCTTCGCGAGTCCAGCCAGTCGCGGAGCACATGCACCGAGGAAACGATC 658
Db 54878 GTCCGCGGACGGTTGCGGTCCAGCCACTCGCCGACCCGCTCGATCCCGGGAATCTGCGG 54819

QY 659 GGGCGGGGATCTGATCAGTCTGGGAGCGGGTCCCGAGCAACCCAGCGTGGGAGCA 718
Db 54818 GCCCGGGTATCCCTCTGCTCTCGGTACGACTCGAGTCTGCCAGCGCAGCGCGGACCTTG 54759

QY 719 CCGAGACCGG--CGCGATGTGCCCGCAGCAGCGCCAGCGCGTGCACCCCGCGGACCG 776
Db 54758 GCGTCCAGAAAGCCCTCCGGTTTGCCTTAATCGGCCAGCCGAGTTCGCGGTAGTCCAG 54699

QY 777 GCGCCCGCGGACCGCGTTCGAGTTCGACCCCGGCC 810
Db 54698 GCGCGGAGCGCGCGATGGCCTTCGACCCCGCAC 54665

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 17:41:32 ; Search time 863 Seconds
(without alignments)
11352.459 Million cell updates/sec

Title: US-10-607-752-115
Perfect score: 1655
Sequence: 1 gatctatctactgaccttc.....atcaccatcaccatcactga 1655

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1655	100.0	1749	5	AAF25122 Nucleotid
2	1011.4	61.1	1749	5	AAF25120 Nucleotid
3	740.2	44.7	1749	5	AAF25121 Nucleotid
4	291	17.6	291	5	AAF25081 Nucleotid
5	261	15.8	261	5	AAF25084 Nucleotid
6	226	13.7	697	5	AAF25080 Nucleotid
7	210	12.7	210	5	AAF25079 Nucleotid
8	177	10.7	177	5	AAF25087 Nucleotid
9	147	8.9	147	5	AAF25082 Nucleotid
10	138	8.3	138	5	AAF25083 Nucleotid
11	132	8.0	132	5	AAF25086 Nucleotid
12	114	6.9	114	5	AAF25077 Nucleotid
13	96	5.8	96	5	AAF25075 Nucleotid
14	95.6	5.8	1245	11	ABD00374 Klebsiell
15	95.6	5.8	1371	11	ABD00219 Klebsiell
16	94.6	5.7	1338	4	AAS53967 Klebsiell
17	87.8	5.3	114955	2	AAx53491 Human ade
18	80	4.8	114955	2	AAx53491 Human ade
19	75	4.5	75	5	AAF25076 Nucleotid
20	69.2	4.2	4725	10	AAD55818 Micromono

C	21	69.2	4.2	60196	10	AAD55810	Aad55810 Micromono
	22	68.4	4.1	1314	5	Aah67646	Aah67646 C glutami
	23	68.4	4.1	1330	4	Aaf71918	Aaf71918 Corynebac
	24	68.4	4.1	1330	4	Aaf72012	Aaf72012 Corynebac
	25	68.4	4.1	1330	4	Aaf71905	Aaf71905 Corynebac
	26	68.4	4.1	1330	4	Aaf71755	Aaf71755 Corynebac
	27	68.4	4.1	1330	4	AAS96078	Aas96078 C. glutam
	28	68.4	4.1	1491	4	Aaf1904	Aaf1904 Corynebac
	29	68.4	4.1	1491	4	Aaf71917	Aaf71917 Corynebac
	30	68.4	4.1	1491	4	Aaf71754	Aaf71754 Corynebac
	31	68.4	4.1	1491	4	Aaf72011	Aaf72011 Corynebac
	32	68.4	4.1	1491	4	AAS96077	Aas96077 C. glutam
	33	68.4	4.1	1498	10	ADD13562	Add13562 C. glutam
	34	68.4	4.1	34980	5	Aah68532	Aah68532 C glutami
	35	66.8	4.0	15624	13	ADQ91707	Adq91707 Polyketid
	36	66.8	4.0	164051	13	ADQ91695	Adq91695 Polyketid
	37	66.2	4.0	1368	13	ADS62019	Ads62019 Bacterial
	38	66.2	4.0	1383	4	AAS51420	Aas51420 Pseudomon
	39	66.2	4.0	1383	8	ACAI9524	Acai9524 Prokaryot
	40	66.2	4.0	1413	11	ABD17125	Abd17125 Pseudomon
	41	66.2	4.0	1527	11	ABD17094	Abd17094 Pseudomon
	42	66.2	4.0	1731	11	ABD17018	Abd17018 Pseudomon
	43	65.2	3.9	1440	8	ACA23916	Aca23916 Prokaryot
	44	64.4	3.9	1209	8	ABX56043	Abx56043 M. echino
	45	63.4	3.8	14055	8	AAL61170	Aal61170 Actinosyn

ALIGNMENTS

RESULT 1
AAF25122
ID AAF25122 standard; DNA; 1749 BP.
XX
AC AAF25122;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of an 8-mer multi-epitope designated ME/D.
XX
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
XX
OS Synthetic.
OS Mycobacterium vaccae.
FH Key Location/Qualifiers
CDS 1..1749
FT /*tag= a
FT /product= "multi-epitope"
XX
XX MOZ00104140-A1.
XX
XX 18-JAN-2001.
XX
XX 10-JUL-2000; 2000WO-NZ000121.
XX
XX 12-JUL-1999; 99US-00351348.
XX 29-NOV-1999; 99US-00450072.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Delcayre A;
XX WPI; 2001-168411/17.
XX P-PSDB; AAB31660.
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX vaccae, useful for treating mycobacterial infections, immune disorders
XX and cancers.
XX Claim 7; Page 68; 80pp; English.
XX

CC The specification describes an immunogenic epitope of a Mycobacterium
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The
 CC epitopes are useful for the treatment of immune disorders, infectious
 CC diseases, especially tuberculosis, and cancer. They are also useful for
 CC treatment of other mycobacterial infections such as those caused by
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
 CC immune responses, and for producing vaccines. The present sequence
 CC encodes an 8-mer multi-epitope designated ME/D
 XX
 SQ Sequence 1749 BP; 275 A; 612 C; 581 G; 281 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1655; DB 5; Length 1749;
 Best Local Similarity 100.0%; Pred. No. 3.3e-297;
 Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 GATCTATCTACTCGACCTTTCGCGACCGGCGGTACCGGGTGGCTGAGTATCTCGGCG 60
 95 GATCTATCTACTCGACCTTTCGCGACCGGCGGTACCGGGTGGCTGAGTATCTCGGCG 154
 61 ATCCGCTGGCGACCGGCTGGCGGTCGCGACGATCAACCGGATGGAAGACGAGGATGG 120
 155 ATCCGCTGGCGACCGGCTGGCGGTCGCGACGATCAACCGGATGGAAGACGAGGATGG 214
 121 TGCCCAAGCTGCCGATCGCGAGCAGGTGCTCGGACCGGTCGCGGATCTCGCGG 180
 215 TGCCCAAGCTGCCGATCGCGAGCAGGTGCTCGGACCGGTCGCGGATCTCGCGG 274
 181 CCGGCAACCTTCGCTCGCGAAGTCCGCGGCTTCGCGGCTTCGCGGCGGATCTGATC 240
 275 CCGGCAACCTTCGCTCGCGAAGTCCGCGGCTTCGCGGCTTCGCGGCGGATCTGATC 334
 241 CAGAACCGGCGGCTTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 300
 335 CAGAACCGGCGGCTTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 394
 301 TCGCGCTGGTATCGCGGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 360
 395 TCGCGCTGGTATCGCGGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 454
 361 GCGCGATGGATCTATCAGTTCGCGGCTTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 420
 455 GCGCGATGGATCTATCAGTTCGCGGCTTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 514
 421 CTCGCGGTCGATCGGCTGGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 480
 515 CTCGCGGTCGATCGGCTGGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 574
 481 GCAACGGGTCGCGGTCGATCTCCAGTCGATGAACGCGGTCGCGGTCGCGGTCGCGG 540
 575 GCAACGGGTCGCGGTCGATCTCCAGTCGATGAACGCGGTCGCGGTCGCGGTCGCGG 634
 541 CCGCGGTCGATCGGCTGGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 600
 635 CCGCGGTCGATCGGCTGGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 694
 601 CGTTCGCGGTCGCGGTCGATCGGCTGGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 660
 695 CGTTCGCGGTCGCGGTCGATCGGCTGGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 754
 661 GCGCGGATCTGATCAGTTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 720
 755 GCGCGGATCTGATCAGTTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 814
 721 GAGACCGGTCGATGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 780
 815 GAGACCGGTCGATGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 874
 781 CCGCGGTCGCGGTCGATGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 840
 875 CCGCGGTCGCGGTCGATGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 934
 841 CAGCGGATGGATCTGATCGGCTGGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 900


Db 935 CACGGATGGATCTGATCGGACGGCATCACGAACAGTAAGCGGTGTTCGGTTGAATCCA 994
 QY 901 AFGTGTGTAGCAGGATTCGATCCCGAAACACGACACGCGAGCAGTTCGCAATCTGTC 960
 Db 995 ATGTGTGTAGCAGGATTCGATCCCGAAACACGACACGCGAGCAGTTCGCAATCTGTC 1054
 QY 961 TCGCACCTGTGCGTCAGCGGTCGTCGCTCCGAAACCGCGCGGATGTCGCGCGG 1020
 Db 1055 TCGCACCTGTGCGTCAGCGGTCGTCGCTCCGAAACCGCGCGGATGTCGCGCGG 1114
 QY 1021 CCGCTGCGGCGCGCTCTCATGCGCGGTCGTCAGTTCGCTCCGCTGGCTGTTCTGCG 1080
 Db 1115 CCGCTGCGGCGCGCTCTCATGCGCGGTCGTCAGTTCGCTCCGCTGGCTGTTCTGCG 1174
 QY 1081 GAAACGGGCGCGCGCTGCTGCTGCGATACGCGGATCTATACGCGAGTTCGCGCGTC 1140
 Db 1175 GAAACGGGCGCGCGCTGCTGCTGCGATACGCGGATCTATACGCGAGTTCGCGCGTC 1234
 QY 1141 CAGCGCTACTCTTCGCGCGGTCGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 1200
 Db 1235 CAGCGCTACTCTTCGCGCGGTCGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 1294
 QY 1201 GCGAGATACACCGACGCGGTCGCTGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 1260
 Db 1295 GCGAGATACACCGACGCGGTCGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 1354
 QY 1261 TGGAGATGGATCTATCGCGCGGTCGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 1320
 Db 1355 TGGAGATGGATCTATCGCGCGGTCGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 1414
 QY 1321 AGTTCGCGCGGTCGCGGTCGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 1380
 Db 1415 AGTTCGCGCGGTCGCGGTCGCTGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGG 1474
 QY 1381 CGTATCTGCGAGTCAGGTTCCCGTCTGCTGCGGTCGCTGCGGTCGCTGCGGTCGCTGCGGTCGCTGCGG 1440
 Db 1475 CGTATCTGCGAGTCAGGTTCCCGTCTGCTGCGGTCGCTGCGGTCGCTGCGGTCGCTGCGGTCGCTGCGG 1534
 QY 1441 CCGGACCGCGTGGATCGTTGCTGAGTACCGGAAAGCTTCGAGAGCTTAAGGCAATTCGG 1500
 Db 1535 CCGGACCGCGTGGATCGTTGCTGAGTACCGGAAAGCTTCGAGAGCTTAAGGCAATTCGG 1594
 QY 1501 AAGATCTTGGACCTTCCCATCAATAGAGGAAAGCATCGCCCTAGGGGATCCGTAGCGG 1560
 Db 1595 AAGATCTTGGACCTTCCCATCAATAGAGGAAAGCATCGCCCTAGGGGATCCGTAGCGG 1654
 QY 1561 GCGCGGTGTTTCGAGTGAACCTTGGGACGGCAATCCCATCGCGGACGCCCGCGAGCGG 1620
 Db 1655 GCGCGGTGTTTCGAGTGAACCTTGGGACGGCAATCCCATCGCGGACGCCCGCGAGCGG 1714
 QY 1621 AATTCACGGATCCCATCACCATCACCATCCTGTA 1655
 Db 1715 AATTCACGGATCCCATCACCATCACCATCCTGTA 1749
 RESULT 2
 AAF25120
 ID AAF25120 standard; DNA; 1749 BP.
 XX
 AC AAF25120;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of an 8-mer multi-epitope designated ME/A.
 XX
 KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
 XX
 OS Synthetic.
 OS Mycobacterium vaccae.
 XX
 FH Key
 FT CDS
 Location/Qualifiers
 1..1749

FT PT CC XX PN XX PD XX PF XX PR XX PA XX PI XX DR XX PT XX CC XX SQ

W0200104140-A1. / *tag= a / product= "multi-epitope"

18-JAN-2001.

10-JUL-2000; 2000WO-NZ000121.

12-JUL-1999. 99US-00351348. 

29-NOV-1999; 99US-00450072.

(GENE-) GENESIS RES & DEV CORP LTD.

Delcayre A;

WPI; 2001-168411/17.

P-PSDB; AAB31658.

Novel polypeptides comprising immunogenic epitopes of Mycobacterium vaccae, useful for treating mycobacterial infections, immune disorders and cancers.

Claim 7; Page 66-67; 80pp; English.

The specification describes an immunogenic epitope of a Mycobacterium vaccae antigen. The epitope is a stimulator of cytokine production. The epitopes are useful for the treatment of immune disorders, infectious diseases, especially tuberculosis, and cancer. They are also useful for treatment of other mycobacterial infections such as those caused by Mycobacterium avium. The epitopes are especially useful for inducing TH1 immune responses, and for producing vaccines. The present sequence encodes an 8-mer multi-epitope designated ME/A

Sequence 1749 BP; 275 A; 612 C; 581 G; 281 T; 0 U; 0 Other;

Query Match 61.1%; Score 1011.4; DB 5; Length 1749;

Best Local Similarity 78.9%; Pred. No. 4.4e-178;

Matches 132; Conservative 0; Mismatches 296; Indels 60; Gaps 8;

Qy 1 GATCTATCTACTCGACCTTCGCCACCGGGGCTACCGGGTGGCTGACCTACTTCGGGCC 60

Db 95 GATCTATCTACTCGACCTTCGCCACCGGGGCTACCGGGTGGCTGACCTACTTCGGGCC 154

Qy 61 ATCCGCTGGGACCGCTCGCGGTTCGGACGATCAACGGATCGAAGAGGAGGATGG 120

Db 155 ATCCGCTGGGACCGCTCGCGGTTCGGACGATCAACGGATCGAAGAGGAGGATGG 214

Qy 121 TGGCCAAACGCTGCCCGATCGGACGAGGTGCTCGGACCGGGTCTCGCGATCTCGCCG 180

Db 215 TGGCCAAACGCTGCCCGATCGGACGAGGTGCTCGGACCGGGTCTCGCGATCTCGCCG 274

Qy 181 CCCGGCACCGTTCGGTTCGGGAACTTCGGCGCTTCGGCGTCTTCGGCGGATCTGATC 240

Db 275 CCCGGCACCGTTCGGTTCGGGAACTTCGGCGCTTCGGCGTCTTCGGCGGATCTGATC 334

Qy 241 CAGAACCGGCGGCTTCGGGTTGAGGTCTCGGTGCGGACGCTCGGTCGACCGACGTCG 300

Db 335 CAGAACCGGCGGCTTCGGGTTGAGGTCTCGGTGCGGACGCTCGGTCGACCGACGTCG 394

Qy 301 TCGGCGCTGGTGATGCGCGCGCTAGCGCTCTCGGTTCACACAGCTCAGCACCGTCCG 360

Db 395 TCGGCGCTGGTGATGCGCGCGCTAGCGCTCTCGGTTCACACAGCTCAGCACCGTCCG 454

Qy 361 GGGCGGATGATCTATCAGTTTCGGCTTCGGTTCGGCGACCGCCCGGAGGCGACGATTCG 420

Db 455 GGGCGGATGATCTATCAGTTTCGGCTTCGGTTCGGCGACGATGAGCGGTTTCGGTTGA 510

Qy 421 CTCGGCGCTCGATCGGGTTGGGTTCGGTTCGGCGACGACACACGATTCACCGCGAGTGA 480

Db 511 TCCAAATGTGCTGTCAGCAGGATCCGA-----TGCCGAAACACCGACCGCAGGATC 564

Qy 481 GCAACGGGTCCCGACCGTGCACATCTCCAGTCGATGAAACCGCGCGAGCTTCGGGGAGT 540

565 GCAATCTGTCTCGCAGACCTTGGCGTCAGCGCGCGTCTGGTCCGCAACCCCGCGCGCAT 624

Qy 541 CGCGCGCAGCAGCAGCGTGTGTTTCAGATGCGACGTTCGCGGTGATGATCCCGGGTTCGGCGT 600

Db 625 GTCCGCGCGCGCGCT-----GCGGCGCGGTCTTCATGGCGGTTCGTTTCAGT 671

Qy 601 CGTCCGGGCTTCGCGCAGTTCAGCCAGTCGCGGAGCACAATGCAACCGACGGGAACGATCCG 660

Db 672 CGCTGTTCGGTGGTGTCTGCGAAAGGCGCGCGCGCGCGCTTCGTCG-----TCCG 724

Qy 661 GCGCGGATCTGATCAGCTTCGGGAGCGGGTTCGCGCAAGCGCGAGCTTCGCGGAGCAGC 720

Db 725 ATACGGGATCTGATCAGCTTCGGGAGCGCGGTTCGCGCAAGCGCGAGCTTCGCGGAGCAGC 784

Qy 721 GAGACCGCGCGATGTCGCGCGCAGCAGCGCGCTGCAACCGCGCGGAGCAGCGCGG 780

Db 785 GAGACCGCGCGATGTCGCGCGCAGCAGCGCGCTGCAACCGCGCGGAGCAGCGCGG 844

Qy 781 CGCGGACCGCTTCGGAGTCGACCCCGCGCGCACCGCGCGCGCTTCGATCAGCATCAGC 840

Db 845 CGCGGACCGCTTCGGAGTCGACCCCGCGCGCACCGCGCGCGCTTCGATCAGCATCAGC 904

Qy 841 CACGGATGATCT-----GATCGCGAGGATCAACGAAAGTAAAGCGGTTCGCGTTGA 896

Db 905 CACGGATGATCTATCAGTTTCGGCGCTTCGCGCGCGCGCGCGGAGCGAGCTTCGCG 964

Qy 897 TCCAAATGCTCTGTCAGCAGCATCCGA-----TGCGGAACACCGACCGCGAGCAGTC 950

Db 965 CTCGGCGCTGATCGGGTTCGGTTCGCGCGCAGCAGCAGCATCCACCGCGAGTTCGA 1024

Qy 951 GCAATCTGTCTCGCAGCCTTCGGCTCAGCGCGCTTCGCTCGCAACCGCGCGCGAT 1010

Db 1025 GCAACGGGTCCCGACCGCTGCAATCTCCAGTCGATGAACCGCGCGAGCTTCGGGAGCT 1084

Qy 1011 GTCCGCGCGCGCT-----GCGCGCGCTCTCCATGCGCGCGGTTCGTTTCAGT 1057

Db 1085 CGCGCGCAGCAGCAGCGTTCGATGCGCAGTTCGCGCTGCAATGATCCCGGGTTCGGCGT 1144

Qy 1058 CGCTCTGCTCGGTGGCTGTTCTGGAACGGCGCGCGCGCGCTTCGCTCG-----TCCG 1110

Db 1145 CGTCCGCGCTTCGCGAGTTCAGCCAGTCGCGGAGCAGATGCAACCGAGGAGCAGCTCG 1204

Qy 1111 ATACGGGATCTATCAGCAGGTAGCGCTTCAGCGCTACTCTTCGCGCCAGAAACAGCGT 1170

Db 1205 GCGCGGATCTATCAGCAGGTAGCGCTTCAGCGCTACTCTTCGCGCCAGAAACAGCGT 1264

Qy 1171 GCGCTCGCGCGCAGACCGCGCTTCGCGCGCAGATACCCAGCGGTTCGCGCGCATG 1230

Db 1265 GCGTCCGCGCGCAGACCGCGCTTCGCGCGCAGATACCCAGCGGTTCGCGCGCATG 1324

Qy 1231 TCCAGATCTGCGCGCGCGCGCGCGCGCGATCGGATCTATCGCGCGGTTCGCG 1290

Db 1325 TCCAGATCTGCGCGCGCGCGCGCGCGCGATCGGATCTATCGCGCGGTTCGCG 1384

Qy 1291 GGAAGACGAGGCGGTAGCGCGCTTCGCTACCTTCGCGCGCGGTTCGCGAGAGCAGGACT 1350

Db 1385 GGAAGACGAGGCGGTAGCGCGCTTCGCTACCTTCGCGCGCGGTTCGCGAGAGCAGGACT 1444

Qy 1351 ACATCGACCGAGCTTCGCGCAACATCGCGCGCTTCGCGCGGTTCGCGGTTCGCGCTTCG 1410

Db 1445 ACATCGACCGAGCTTCGCGCAACATCGCGCGCTTCGCGCGGTTCGCGGTTCGCGCTTCG 1504

Qy 1411 TCGGATCTATCG 1470

Db 1505 TCGGATCTATCG 1564

Qy 1471 CGAAGCTCTTGAGAGCTTAAGCCAAATGGAAGATCTTCGAGCTTCCTCCATCATAGAGG 1530

Db 1565 CGAAGCTCTTGAGAGCTTAAGCCAAATGGAAGATCTTCGAGCTTCCTCCATCATAGAGG 1624

Qy 1531 AAAAGCATCCCTTAGGGGATTCGATGCGCGCGCGGTTCGAGTGAACTTCGGGAGGG 1590

Db 1625 AAAAGCATCCCTAGGGATCCGTAGCGGCCCGGTGTTTCAGTGAACATTGGGCGAGG 1684
 QY 1591 CAATCCCATCGCGCGAGCCCGCGCGGCGGAAATCCACGGATCCCATACCATCACCATC 1650
 Db 1685 CAATCCCATCGCGCGAGCCCGCGCGGCGGAAATCCACGGATCCCATACCATCACCATC 1744
 QY 1651 ACTGA 1655
 Db 1745 ACTGA 1749

RESULT 3

AAF25121

ID AAF25121 standard; DNA; 1749 BP.

XX AC

AAF25121;

30-APR-2001 (first entry)

DE Nucleotide sequence of an 8-mer multi-epitope designated ME/B.

XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
 XX OS

XX Synthetic.

XX Mycobacterium vaccae.

XX Key Location/Qualifiers
 FH 1.1749
 FT CDS /*tag= a
 FT /product= "multi-epitope"

XX WO200104140-A1.
 XX 18-JAN-2001.
 XX 10-JUL-2000; 2000WO-NZ000121.
 XX 12-JUL-1999; 99US-00351348.
 PR 29-NOV-1999; 99US-00450072.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA Delcayre A;
 XX WPI; 2001-168411/17.
 PI P-PSDB; AAB31659.

XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
 PT vaccae, useful for treating mycobacterial infections, immune disorders
 PT and cancers.

XX Claim 7; Page 67; 80pp; English.

XX The specification describes an immunogenic epitope of a Mycobacterium
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The
 CC epitopes are useful for the treatment of immune disorders, infectious
 CC diseases, especially tuberculosis, and cancer. They are also useful for
 CC treatment of other mycobacterial infections such as those caused by
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
 CC immune responses, and for producing vaccines. The present sequence
 CC encodes an 8-mer multi-epitope designated ME/B

XX Sequence 1749 BP; 275 A; 612 C; 581 G; 281 T; 0 U; 0 Other;

Query Match 44.7%; Score 740.2; DB 5; Length 1749;

Best Local Similarity 69.0%; Pred. No. 6.9e-128;

Matches 1244; Conservative 0; Mismatches 263; Indels 296; Gaps 5;

QY 1 GATCTATCTACTCGACCTTCGCGACCGGCGGTACCGGGTGGCTGACGTACTCGGCC 60

Db 95 GATCTATCTACTCGACCTTCGCGACCGGCGGTACCGGGTGGCTGACGTACTCGGCC 154

QY 61 ATCCGCTGGCGACCCGCTAGCGGCTCGCGACGATCAACGCGATGGAAGACGAAGCATGG 120
 Db 155 ATCCGCTGGCGACCCGCTAGCGGCTCGCGACGATCAACGCGATGGAAGACGAAGCATGG 214
 QY 121 TGGCCAAACGCTCCCGCATCGCGGACGAGGTGCTCGGACCGGGTCTGCGCGATCTCGCG 180
 Db 215 TGGCCAAACGCTCCCGCATCGCGGACGAGGTGCTCGGACCGGGTCTGCGCGATCTCGCG 274
 QY 181 CCGCGACCGTTCCGTCGGCGAAGTCCGCGGCTCGGCGTCTTCTGGGGGGGATCTGATC 240
 Db 275 CCGCGACCGTTCCGTCGGCGAAGTCCGCGGCTCGGCGTCTTCTGGGGG----- 324
 QY 241 CAGAACGGGCGGTCTGCGGGTTGAGGTCCTCGGTGCCCAGTGCCGTGACGCGAGCTCG 300
 Db 325 ----- 324
 QY 301 TCGGCGCTGTGATCGGCGCGCTAGGCGTCTCGGTCCAACGTCAGCACCGTGCCTC 360
 Db 325 ----- 324
 QY 361 GGGCGGATGGATCTATCAGTTCCGGCCCTGGTCCGACGCCCGCGAGGGGAGCAGTTCGG 420
 Db 325 -----GGATCTATCAGTTCCGGCCCTGGTCCGACGCCCGCGAGGGGAGCAGTTCGG 376
 QY 421 CTCGGCGTCGATCGGTTGGGTCCGTCCGGCAGCACACACGATCCACCCGAGGTCCA 480
 Db 377 CTCGGCGTCGATCGGTTGGGTCCGTCCGGCAGCACACACGATCCACCCGAGGTCCA 436
 QY 481 GCACGGGTCCCGACGGTGCACATCTCCAGTCCGATGAACCCCGAGCTCGGGACGT 540
 Db 437 GCACGGGTCCCGACGGTGCACATCTCCAGTCCGATGAACCCCGAGCTCGGGACGT 496
 QY 541 CCGGGCGCAGCAGCAGTGTTCAGATGGCAGTCCCGTGCATGATCCCGGTTCCGGCT 600
 Db 497 CCGGGCGCAGCAGCAGTGTTCAGATGGCAGTCCCGTGCATGATCCCGGTTCCGGCT 556
 QY 601 CGTCGGGCTCGCGAGTCCAGCCAGTCCGCGAGCACATGACACCGAGGAACTCGG 660
 Db 557 CGTCGGGCTCGCGAGTCCAGCCAGTCCGCGAGCACATGACACCGAGGAACTCGG 616
 QY 661 GCGCGGGATCTGATCAGTCCGGGAGCCGGTGCACGACCGCAGCGTGGGAAACAC 720
 Db 617 GCGCGGGATCTGATC-----GGCAGGCATCACGAAACAGTAAGCGGTCTTCGGTT 666
 QY 721 GAGACGGGCGCATGTGCCCGCAGCAGCGCCAGCGGTGACACCCCGGAGACCGGCC 780
 Db 667 GAATCCAAATGTCTGTTCAGCAGGCGATCCGATCCGAAACACCGACCGAGCATGCG 726
 QY 781 CCGCGGACCGCGTCGGAGTCCGACCCCGCGCCACCGCGCGCGGTGTGTCAGCATCAGC 840
 Db 727 ATCTGTCTCGACACCTTGGGTCACGCGGGTCTCGTGGTCCGCAACCCCGCGCATGTC 786
 QY 841 CACGGGATGGATCTGATCGGACGGC---ATCAGAACAGTAAGCGGTGTTCGGTTGAAT 897
 Db 787 GCGCGCGCGCTCGCGCGCGCTCTCCATGGCCGGTTCGTTTCAGTGGCTCGTCCGCTGGCT 846
 QY 898 CCAATGTGTGTTCAGCAGCATCCGATGCCGAAACCGACACCGCGAGCAGTTCGCAATCT 957
 Db 847 GTTCTCGAAACCGGGCCCGCGCCCGCTCGTCCGATACCGGATCTGATCAGTCTCGGG 906
 QY 958 GTTCTCGCAACCTGGCGTCAACCGCGCTCGTGGCTCCGCAACCCCGCGCGATGTCCGCG 1017
 Db 907 GAGCGGGTGGCCGAGCAACCGCGTCGGGAAACCGAGACCGGGCGCATGTGCCCGCG 966
 QY 1018 GCGCGCTGCGCGCGCTCTCCATGGCCGGTTCGTTTCAGTGGCTCGTCCGGTGGCTGTTTC 1077
 Db 967 CAGCAGCGCCACAGCGGTGACCCCGCGGACCGGGCCCGCGGACCGCGTCCGGAGTTCGAC 1026
 QY 1078 TCGGAAACGGGCGCGCGCC-----CGTGTCTCGTCCGATACCGGATCTATCAGCGCAG 1130
 Db 1027 CCGGGCGCCACCGCGCGCGGTGTGATGATACCGACCGGGATGATCTATCAGCGCAG 1086
 QY 1131 GTAGGCGGTCCAGCCGTACTCTTCGCCCCAGAACAGCGGTGCCGTGCGCGCGACGACCG 1190

Db 1087 GTAGGCGGTCCAGCGTACTTTCGCGCCAGAACAGCGGTGCGCGTCCGCGCAGACCG 1146
 Qy 1191 CGGTCTCGCGCCAGATACACCCAGGCGGTGGCGGCATGTCCAGATCGTGGCCAGCGG 1250
 Db 1147 CGGTCTCGCGCCAGATACACCCAGGCGGTGGCGGCATGTCCAGATCGTGGCCAGCGG 1206
 Qy 1251 CGCGGACCGGTGAGATCGGATCTATCGCGCGCTGTGGGGAAGACGAGGCGGTAGCG 1310
 Db 1207 CGCGGACCGGTGAGATCGGATCTATCGCGCGCTGTGGGGAAGACGAGGCGGTAGCG 1266
 Qy 1311 GCGTTGCACTACGTGCGCGCGGTGGCGGAAGACGAGATACATCGACGAGCCTTGGCG 1370
 Db 1267 GCGTTGCACTACGTGCGCGCGGTGGCGGAAGACGAGATACATCGACGAGCCTTGGCG 1326
 Qy 1371 AACATCGCGCGCTATCGGAGCTGAGTTCGCGCTCTCGTGGT----- 1413
 Db 1327 AACATCGCGCGCTATCGGAGCTGAGTTCGCGCTCTCGTGGT----- 1413
 Qy 1414 ----- 1413
 Db 1387 GCCGCTCGCGGTGAGTTCCTCGGTGCCAGTGCCTGCGTCCAGCGGCGTCTCGGCGT 1446
 Qy 1414 ----- 1413
 Db 1447 GGTGATCGCGCGCGGTAGCGTCTCGGTCCAGACGTGCGTCCAGCGGCGGAT 1506
 Qy 1414 -GATCTATCGCGCCAGCGCGCGGTGCGCGGCAACCGTGGATCGTTCAGTACCGG 1472
 Db 1507 GGTATCTATCGCGCGCGGTGCGCGGCAACCGTGGATCGTTCAGTACCGG 1566
 Qy 1473 AAGCTCTTGAGAGCTAAGGCAATTGGGAAGATCTTGGACCTTCCATCAATAGAGGAA 1532
 Db 1567 AAGCTCTTGAGAGCTAAGGCAATTGGGAAGATCTTGGACCTTCCATCAATAGAGGAA 1626
 Qy 1533 AAGCATCGCCCTAGGGGATCCGTAGCGGCGCGCGGTGTTTCGAGTGAATTTGGGCGAGGCA 1592
 Db 1627 AAGCATCGCCCTAGGGGATCCGTAGCGGCGCGCGGTGTTTCGAGTGAATTTGGGCGAGGCA 1686
 Qy 1593 ATCCCATCGCGCGAGCGCGGCAACCGGAAATCCAGGATCCCATCAGCATCACCATCAC 1652
 Db 1687 ATCCCATCGCGCGAGCGCGGCAACCGGAAATCCAGGATCCCATCAGCATCACCATCAC 1746
 Qy 1653 TGA 1655
 Db 1747 TGA 1749

RESULT 4
 AAF25081
 AAF25081 standard; DNA; 291 BP.

AC AAF25081;
 DT 30-APR-2001 (first entry)
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA26.
 XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
 XX Mycobacterium vaccae.
 OS
 XX WO200104140-A1.
 FN
 XX 18-JAN-2001.
 PD
 XX 10-JUL-2000; 2000WO-NZ000121.
 PF
 XX 12-JUL-1999; 99US-00351348.
 PR 29-NOV-1999; 99US-00450072.
 XX
 XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;
 PI
 XX WPI: 2001-168411/17.
 DR P-PSDB; AAB31651.
 XX
 PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium
 PT vaccae, useful for treating mycobacterial infections, immune disorders
 PT and cancers.
 XX
 XX Claim 4; Page 59; 80pp; English.
 PS
 XX The specification describes an immunogenic epitope of a Mycobacterium
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The
 CC epitopes are useful for the treatment of immune disorders, infectious
 CC diseases, especially tuberculosis, and cancer. They are also useful for
 CC treatment of other mycobacterial infections such as those caused by
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
 CC immune responses, and for producing vaccines. The present sequence
 CC encodes a M. vaccae epitope of the invention
 XX
 SQ Sequence 291 BP; 45 A; 103 C; 101 G; 42 T; 0 U; 0 Other;
 Query Match 17.6%; Score 291; DB 5; Length 291;
 Best Local Similarity 100.0%; Pred. No. 9.6e-45;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 375 ATCAGTTCCGCGCTGTCGCCAGCGCGGAGGCGAGCCAGTTCCGCTCCGGGTCGATC 434
 Db 1 ATCAGTTCCGCGCTGTCGCCAGCGCGGAGGCGAGCCAGTTCCGCTCCGGGTCGATC 60
 Qy 435 GGGTTGGGTCGCTCCGCGCAGCACACAGCATCCACCGAGGTCGAGCAACGGGTCCCG 494
 Db 61 GGGTTGGGTCGCTCCGCGCAGCACACAGCATCCACCGAGGTCGAGCAACGGGTCCCG 120
 Qy 495 ACGGTGCATCTCCAGTCGATGAACCGCGCGAGCTCCGGGACGTCGCGCGCAGCAGC 554
 Db 121 ACGGTGCATCTCCAGTCGATGAACCGCGCGAGCTCCGGGACGTCGCGCGCAGCAGC 180
 Qy 555 ACGTTGTCAGATGGCAGTCGCGCTGTCATGATCCCGGTTTCGCGGCTCGGCTCGCG 614
 Db 181 ACGTTGTCAGATGGCAGTCGCGCTGTCATGATCCCGGTTTCGCGGCTCGGCTCGCG 240
 Qy 615 GAGTCCAGCGAGTCGCGGAGCACATGACCGAGGAAACGACTCGGCGCGG 665
 Db 241 GAGTCCAGCGAGTCGCGGAGCACATGACCGAGGAAACGACTCGGCGCGG 291

RESULT 5
 AAF25084
 ID AAF25084 standard; DNA; 261 BP.
 XX
 AC AAF25084;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA37.
 XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
 XX Mycobacterium vaccae.
 OS
 XX WO200104140-A1.
 FN
 XX 18-JAN-2001.
 PD
 XX 10-JUL-2000; 2000WO-NZ000121.
 PF
 XX 12-JUL-1999; 99US-00351348.
 PR 29-NOV-1999; 99US-00450072.
 XX
 XX (GENE-) GENESIS RES & DEV CORP LTD.

```

XX PI Delcayre A;
XX PR WPI; 2001-168411/17.
XX DR P-PSDB; AAB31653.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Delcayre A;
XX DR WPI; 2001-168411/17.
XX DR P-PSDB; AAB31649.
XX PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX PT vaccae, useful for treating mycobacterial infections, immune disorders
XX PT and cancers.
XX PS Claim 4; Page 60; 80pp; English.
XX CC The specification describes an immunogenic epitope of a Mycobacterium
XX CC vaccae antigen. The epitope is a stimulator of cytokine production. The
XX CC epitopes are useful for the treatment of immune disorders, infectious
XX CC diseases, especially tuberculosis, and cancer. They are also useful for
XX CC treatment of other mycobacterial infections such as those caused by
XX CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX CC immune responses, and for producing vaccines. The present sequence
XX CC encodes a M. vaccae epitope of the invention.
XX SQ Sequence 261 BP; 37 A; 94 C; 83 G; 47 T; 0 U; 0 Other;
XX
XX Query Match 15.8%; Score 261; DB 5; Length 261;
XX Best Local Similarity 100.0%; Pred. No. 3.4e-39;
XX Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 855 GATCGGCAGGCATCACGAAACAGTAAAGCGGTGTTCCGGTTGAATCCAAATGCTGTGTCAGCA 914
XX Db 1 GATCGGCAGGCATCACGAAACAGTAAAGCGGTGTTCCGGTTGAATCCAAATGCTGTGTCAGCA 60
XX
XX QY 915 GGCATCCGATGCCGAACACCGACACGAGCAGTGCCTGCTGTCGGACCTTGGCG 974
XX Db 61 GGCATCCGATGCCGAACACCGACACGAGCAGTGCCTGCTGTCGGACCTTGGCG 120
XX
XX QY 975 TCACGGCGGTGCTGGTTCGCAACCCGCGCGGATGTCGCGCGCGCGCTGGCGCGC 1034
XX Db 121 TCACGGCGGTGCTGGTTCGCAACCCGCGCGGATGTCGCGCGCGCGCTGGCGCGC 180
XX
XX QY 1035 TCTCCATGGCGGTGCTGTTCAAGTCGTCGTCGGTGGCTGTTCTGCGAAACGGGCCCGCG 1094
XX Db 181 TCTCCATGGCGGTGCTGTTCAAGTCGTCGTCGGTGGCTGTTCTGCGAAACGGGCCCGCG 240
XX
XX QY 1095 CCCCGTCGTCGTCGATAGC 1115
XX 241 CCCCGTCGTCGTCGATAGC 261
XX
XX RESULT 6
XX AAF25080
XX ID AAF25080 standard; DNA; 697 BP.
XX AC AAF25080;
XX DT 30-APR-2001 (first entry)
XX DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA9A.
XX KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
XX KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
XX OS Mycobacterium vaccae.
XX FH Key Location/Qualifiers
XX FT CDS 1..225
XX FT /*tag= a
XX FT /note= "no termination sequence given"
XX FT
XX PN WO200104140-A1.
XX XX
XX PD 18-JAN-2001.
XX PR 10-JUL-2000; 2000WO-NZ000121.
XX PF

```

```

XX XX 12-JUL-1999; 99US-00351348.
XX PR 29-NOV-1999; 99US-00450072.
XX XX
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Delcayre A;
XX DR WPI; 2001-168411/17.
XX DR P-PSDB; AAB31649.
XX PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX PT vaccae, useful for treating mycobacterial infections, immune disorders
XX PT and cancers.
XX PS Claim 4; Page 59; 80pp; English.
XX CC The specification describes an immunogenic epitope of a Mycobacterium
XX CC vaccae antigen. The epitope is a stimulator of cytokine production. The
XX CC epitopes are useful for the treatment of immune disorders, infectious
XX CC diseases, especially tuberculosis, and cancer. They are also useful for
XX CC treatment of other mycobacterial infections such as those caused by
XX CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX CC immune responses, and for producing vaccines. The present sequence
XX CC encodes a M. vaccae epitope of the invention.
XX SQ Sequence 697 BP; 89 A; 253 C; 253 G; 102 T; 0 U; 0 Other;
XX
XX Query Match 13.7%; Score 226; DB 5; Length 697;
XX Best Local Similarity 100.0%; Pred. No. 1e-32;
XX Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 ATCTACTGACCTTCGCGACCGCGGTACCCGGTGGCTGACGTACTCCGGCCATCG 65
XX Db 1 ATCTACTGACCTTCGCGACCGCGGTACCCGGTGGCTGACGTACTCCGGCCATCG 60
XX
XX QY 66 CTGGCGACCGCTGCGCGTCCGACGATCAACGCGATGGAAGACGAAGGCATGGTGCC 125
XX Db 61 CTGGCGACCGCTGCGCGTCCGACGATCAACGCGATGGAAGACGAAGGCATGGTGCC 120
XX
XX QY 126 AACGCTGCGCGCATCGCGAGCAGGTGCTCGGACCGGGTCTCGCGATCTCCCGCCCG 185
XX Db 121 AACGCTGCGCGCATCGCGAGCAGGTGCTCGGACCGGGTCTCGCGATCTCCCGCCCG 180
XX
XX QY 186 CACCGTTCGTCGCGAAGTCCGCGCTCGCGCTCTTCGGCGCG 231
XX Db 181 CACCGTTCGTCGCGAAGTCCGCGCTCGCGCTCTTCGGCGCG 226
XX
XX RESULT 7
XX AAF25079
XX ID AAF25079 standard; DNA; 210 BP.
XX AC AAF25079;
XX DT 30-APR-2001 (first entry)
XX DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA5.
XX KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
XX KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
XX OS Mycobacterium vaccae.
XX FH Key Location/Qualifiers
XX FT CDS 1..225
XX FT /*tag= a
XX FT /note= "no termination sequence given"
XX FT
XX PN WO200104140-A1.
XX XX
XX PD 18-JAN-2001.
XX PR 10-JUL-2000; 2000WO-NZ000121.
XX PF
XX XX 12-JUL-1999; 99US-00351348.
XX PR 29-NOV-1999; 99US-00450072.
XX XX

```

PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX Delcayre A;
 PI WPI; 2001-168411/17.
 DR P-PSDB; AAB31648.
 XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
 PT vaccae, useful for treating mycobacterial infections, immune disorders
 PT and cancers.
 XX Claim 4; Page 59; 80pp; English.
 PS The specification describes an immunogenic epitope of a Mycobacterium
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The
 CC epitopes are useful for the treatment of immune disorders, infectious
 CC diseases, especially tuberculosis, and cancer. They are also useful for
 CC treatment of other mycobacterial infections such as those caused by
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
 CC immune responses, and for producing vaccines. The present sequence
 CC encodes a M. vaccae epitope of the invention
 XX Sequence 210 BP; 45 A; 66 C; 64 G; 35 T; 0 U; 0 Other;
 SQ
 Query Match 12.7%; Score 210; DB 5; Length 210;
 Best Local Similarity 100.0%; Pred. No. 9.4e-30;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1419 ATCGCGCCACCGCGCGTGCCTGGGACCGCGTGGATCGTTCAGTACCCGAAAGCTC 1478
 Db 1 ATCGCGCCACCGCGCGTGCCTGGGACCGCGTGGATCGTTCAGTACCCGAAAGCTC 60
 QY 1479 TTGAGAGCTAAGGCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGGAAAGCAT 1538
 Db 61 TTGAGAGCTAAGGCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGGAAAGCAT 120
 QY 1539 CGCCTAGGGGATCCGTAGCGGGCCCGTGTTCGAGTGAATTTGGCGAGGCAATCCCA 1598
 Db 121 CGCCTAGGGGATCCGTAGCGGGCCCGTGTTCGAGTGAATTTGGCGAGGCAATCCCA 180
 QY 1599 TCGCGCGCAGCGCGCGAGCGGAATCCAC 1628
 Db 181 TCGCGCGCAGCGCGCGAGCGGAATCCAC 210
 RESULT 8
 AAF25087
 ID AAF25087 standard; DNA; 177 BP.
 XX AAF25087;
 XX 30-APR-2001 (first entry)
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA45.
 XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
 XX Mycobacterium vaccae.
 OS WO200104140-A1.
 PN 18-JAN-2001.
 PD 10-JUL-2000; 2000WO-NZ000121.
 PP 12-JUL-1999; 99US-00351348.
 PR 29-NOV-1999; 99US-00450072.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA Delcayre A;
 PI WPI; 2001-168411/17.
 DR P-PSDB; AAB31651.
 XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
 PT vaccae, useful for treating mycobacterial infections, immune disorders
 PT and cancers.
 XX Claim 4; Page 59; 80pp; English.
 PS The specification describes an immunogenic epitope of a Mycobacterium
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The
 CC epitopes are useful for the treatment of immune disorders, infectious
 CC diseases, especially tuberculosis, and cancer. They are also useful for
 CC treatment of other mycobacterial infections such as those caused by
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
 CC immune responses, and for producing vaccines. The present sequence
 CC encodes a M. vaccae epitope of the invention
 XX Sequence 210 BP; 45 A; 66 C; 64 G; 35 T; 0 U; 0 Other;
 SQ
 Query Match 12.7%; Score 210; DB 5; Length 210;
 Best Local Similarity 100.0%; Pred. No. 9.4e-30;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1419 ATCGCGCCACCGCGCGTGCCTGGGACCGCGTGGATCGTTCAGTACCCGAAAGCTC 1478
 Db 1 ATCGCGCCACCGCGCGTGCCTGGGACCGCGTGGATCGTTCAGTACCCGAAAGCTC 60
 QY 1479 TTGAGAGCTAAGGCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGGAAAGCAT 1538
 Db 61 TTGAGAGCTAAGGCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGGAAAGCAT 120
 QY 1539 CGCCTAGGGGATCCGTAGCGGGCCCGTGTTCGAGTGAATTTGGCGAGGCAATCCCA 1598
 Db 121 CGCCTAGGGGATCCGTAGCGGGCCCGTGTTCGAGTGAATTTGGCGAGGCAATCCCA 180
 QY 1599 TCGCGCGCAGCGCGCGAGCGGAATCCAC 1628
 Db 181 TCGCGCGCAGCGCGCGAGCGGAATCCAC 210
 RESULT 8
 AAF25087
 ID AAF25087 standard; DNA; 177 BP.
 XX AAF25087;
 XX 30-APR-2001 (first entry)
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA45.
 XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
 XX Mycobacterium vaccae.
 OS WO200104140-A1.
 PN 18-JAN-2001.
 PD 10-JUL-2000; 2000WO-NZ000121.
 PP 12-JUL-1999; 99US-00351348.
 PR 29-NOV-1999; 99US-00450072.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA Delcayre A;
 PI WPI; 2001-168411/17.
 DR P-PSDB; AAB31651.
 XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
 PT vaccae, useful for treating mycobacterial infections, immune disorders
 PT and cancers.
 XX Claim 4; Page 59; 80pp; English.

DR WPI; 2001-168411/17.
 XX P-PSDB; AAB31656.
 PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium
 PT vaccae, useful for treating mycobacterial infections, immune disorders
 PT and cancers.
 XX Claim 4; Page 60; 80pp; English.
 PS The specification describes an immunogenic epitope of a Mycobacterium
 CC vaccae antigen. The epitope is a stimulator of cytokine production. The
 CC epitopes are useful for the treatment of immune disorders, infectious
 CC diseases, especially tuberculosis, and cancer. They are also useful for
 CC treatment of other mycobacterial infections such as those caused by
 CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
 CC immune responses, and for producing vaccines. The present sequence
 CC encodes a M. vaccae epitope of the invention
 XX Sequence 177 BP; 27 A; 71 C; 66 G; 13 T; 0 U; 0 Other;
 SQ
 Query Match 10.7%; Score 177; DB 5; Length 177;
 Best Local Similarity 100.0%; Pred. No. 1.2e-23;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 672 GATCAGCTCGGGAGCGCGTGCCTCCAGCAACGCCAGCTGGGAGCACCAGACCGCGCGC 731
 Db 1 GATCAGCTCGGGAGCGCGTGCCTCCAGCAACGCCAGCTGGGAGCACCAGACCGCGCGC 60
 QY 732 GATGTCGCGCGCAGCAGCGCGCCAGCGCTGCACCCCGCGGACCGCGCGCGCGGAT 791
 Db 61 GATGTCGCGCGCAGCAGCGCGCCAGCGCTGCACCCCGCGGACCGCGCGCGCGGAT 120
 QY 792 GTCGGAGTGCACCCCGCGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGGAT 848
 Db 121 GTCGGAGTGCACCCCGCGCGCCACCGCGCGCGCGCGCGCGCGCGCGCGCGGAT 177
 RESULT 9
 AAF25082
 ID AAF25082 standard; DNA; 147 BP.
 XX AAF25082;
 XX 30-APR-2001 (first entry)
 DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA27.
 XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
 XX Mycobacterium vaccae.
 OS WO200104140-A1.
 PN 18-JAN-2001.
 PD 10-JUL-2000; 2000WO-NZ000121.
 PP 12-JUL-1999; 99US-00351348.
 PR 29-NOV-1999; 99US-00450072.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA Delcayre A;
 PI WPI; 2001-168411/17.
 DR P-PSDB; AAB31651.
 XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
 PT vaccae, useful for treating mycobacterial infections, immune disorders
 PT and cancers.
 XX Claim 4; Page 59; 80pp; English.

XX The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC encodes a M. vaccae epitope of the invention

XX Sequence 147 BP; 25 A; 54 C; 49 G; 19 T; 0 U; 0 Other;
SQ

Query Match 8.9%; Score 147; DB 5; Length 147;
Best Local Similarity 100.0%; Pred. No. 4.3e-18;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1122 ATCAGCAGGTAGGCGGTCCAGCGGTACTTTCGCCCCAGAAACAGCGGTGCCGTCCCGC 1181
|||
1 ATCAGCAGGTAGGCGGTCCAGCGGTACTTTCGCCCCAGAAACAGCGGTGCCGTCCCGC 60

QY 1182 GCAGACGCGGTCTCTCCGCCAGATACACCCAGCGGTGGCCGATGTCCAGATCGTG 1241
|||
61 GCAGACGCGGTCTCTCCGCCAGATACACCCAGCGGTGGCCGATGTCCAGATCGTG 120

QY 1242 GCCAGCGCGCGCGCACGGTGGAGATC 1268
|||
121 GCCAGCGCGCGCGCACGGTGGAGATC 147

RESULT 10
AAF25083
ID AAF25083 standard; DNA; 138 BP.
XX
AC AAF25083;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA29.
XX
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
XX
OS Mycobacterium vaccae.
XX
PN WO200104140-A1.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-NZ000121.
XX
PR 12-JUL-1999; 99US-00351348.
PR 29-NOV-1999; 99US-00450072.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Delcayre A;
XX
DR WPI; 2001-168411/17.
DR P-PSDB; AAB31652.
XX
PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX
PS Claim 4; Page 60; 80pp; English.
XX
CC The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC encodes a M. vaccae epitope of the invention

CC encodes a M. vaccae epitope of the invention
XX
SQ Sequence 138 BP; 23 A; 44 C; 47 G; 24 T; 0 U; 0 Other;
Query Match 8.3%; Score 138; DB 5; Length 138;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1275 ATCGCGCGCTGTGGGGAAGACGAGCGGTAGCGGCTTGCACTACGTGCGCCGGTT 1334
|||
1 ATCGCGCGCTGTGGGGAAGACGAGCGGTAGCGGCTTGCACTACGTGCGCCGGTT 60

DB 1335 GCGGAGAAGCAGACTACATCGACCGAGCTTTCGCAACATCGGGCGGTATCTGCCAGCT 1394
|||
61 GCGGAGAAGCAGACTACATCGACCGAGCTTTCGCAACATCGGGCGGTATCTGCCAGCT 120

QY 1395 GAGGTTCCCGCTCTCGTC 1412
|||
121 GAGGTTCCCGCTCTCGTC 138

RESULT 11
AAF25086
ID AAF25086 standard; DNA; 132 BP.
XX
AC AAF25086;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of a M. vaccae immunogenic epitope from DNA44.
XX
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.
XX
OS Mycobacterium vaccae.
XX
PN WO200104140-A1.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-NZ000121.
XX
PR 12-JUL-1999; 99US-00351348.
PR 29-NOV-1999; 99US-00450072.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Delcayre A;
XX
DR WPI; 2001-168411/17.
DR P-PSDB; AAB31655.
XX
PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX
PS Claim 4; Page 60; 80pp; English.
XX
CC The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC encodes a M. vaccae epitope of the invention

XX Sequence 132 BP; 16 A; 44 C; 50 G; 22 T; 0 U; 0 Other;
SQ

Query Match 8.0%; Score 132; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 2.6e-15;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 GATCCAGACGGCCGGTCTGCGGGTTGAGTCTCGGTGCGCCAGTGGCGGTGCGACGCGAC 296
DB 1 GATCCAGAACGGCCCGGTCTGCGGGTTGAGGTCTCGGTGCGCCAGTGGCGGTGCGACGCGAC 60

QY 297 GTCTGCGGCGTGGTGTATGCGGCGCGGTAGGCGTCTCGGTCCACAAAGTCCAGCACCGT 356
DB 61 GTCTGCGGCGTGGTGTATGCGGCGCGGTAGGCGTCTCGGTCCACAAAGTCCAGCACCGT 120

QY 357 GCCCGGCGGAT 368
DB 121 GCCCGGCGGAT 132

RESULT 12

AAF25077
ID AAF25077 standard; DNA; 114 BP.

AC AAF25077;

XX AAF25077;

XX 30-APR-2001 (first entry)

DT 30-APR-2001 (first entry)

XX Nucleotide sequence of a M. vaccae immunogenic epitope from DNA27.

XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.

XX Mycobacterium vaccae.

OS WO200104140-A1.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-NZ000121.

XX 12-JUL-1999; 99US-00351348.

XX 29-NOV-1999; 99US-00450072.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;

XX WPI; 2001-168411/17.

XX P-PSDB; AAB31646.

XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX Claim 4; Page 58; 80pp; English.

PS The specification describes an immunogenic epitope of a Mycobacterium
XX vaccae antigen. The epitope is a stimulator of cytokine production. The
XX epitopes are useful for the treatment of immune disorders, infectious
XX diseases, especially tuberculosis, and cancer. They are also useful for
XX treatment of other mycobacterial infections such as those caused by
XX Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX immune responses, and for producing vaccines. The present sequence
XX encodes a M. vaccae epitope of the invention

XX Sequence 114 BP; 20 A; 44 C; 35 G; 15 T; 0 U; 0 Other;

QY 1122 ATCAGCAGGTAGGCGGTCCAGCGTACTCTTCGCCCGCAGAACAGCGGTGCGTCGCGC 1181
DB 1 ATCAGCAGGTAGGCGGTCCAGCGTACTCTTCGCCCGCAGAACAGCGGTGCGTCGCGC 60
QY 1182 GCAGACGCGGTCTCTGCGCGCAGATACACCGCGGTGCGCGCATGTCGAG 1235
DB 61 GCAGACGCGGTCTCTGCGCGCAGATACACCGCGGTGCGCGCATGTCGAG 114

Query Match 6.9%; Score 114; DB 5; Length 114;

Best Local Similarity 100.0%; Pred. No. 5.5e-12;

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1122 ATCAGCAGGTAGGCGGTCCAGCGTACTCTTCGCCCGCAGAACAGCGGTGCGTCGCGC 1181

DB 1 ATCAGCAGGTAGGCGGTCCAGCGTACTCTTCGCCCGCAGAACAGCGGTGCGTCGCGC 60

QY 1182 GCAGACGCGGTCTCTGCGCGCAGATACACCGCGGTGCGCGCATGTCGAG 1235

DB 61 GCAGACGCGGTCTCTGCGCGCAGATACACCGCGGTGCGCGCATGTCGAG 114

RESULT 13

AAF25075
ID AAF25075 standard; DNA; 96 BP.

XX AAF25075;

XX AAF25075;

XX 30-APR-2001 (first entry)

DT 30-APR-2001 (first entry)

XX Nucleotide sequence of a M. vaccae immunogenic epitope from DNA5.

XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine; ss.

XX Mycobacterium vaccae.

OS WO200104140-A1.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-NZ000121.

XX 12-JUL-1999; 99US-00351348.

XX 29-NOV-1999; 99US-00450072.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;

XX WPI; 2001-168411/17.

XX P-PSDB; AAB31644.

XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX Claim 4; Page 58; 80pp; English.

XX The specification describes an immunogenic epitope of a Mycobacterium
XX vaccae antigen. The epitope is a stimulator of cytokine production. The
XX epitopes are useful for the treatment of immune disorders, infectious
XX diseases, especially tuberculosis, and cancer. They are also useful for
XX treatment of other mycobacterial infections such as those caused by
XX Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX immune responses, and for producing vaccines. The present sequence
XX encodes a M. vaccae epitope of the invention

XX Sequence 96 BP; 27 A; 24 C; 25 G; 20 T; 0 U; 0 Other;

Query Match 5.8%; Score 96; DB 5; Length 96;

Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1458 GTTCGTGACGACCGGAGCTCTTGAGAGCTTAAGGCAATTGGGAAGATCTTGACCTTC 1517

DB 1 GTTCGTGACGACCGGAGCTCTTGAGAGCTTAAGGCAATTGGGAAGATCTTGACCTTC 60

QY 1518 CCATCAATAGAGAAAGCATCCCTTAGGGATCC 1553

DB 61 CCATCAATAGAGAAAGCATCCCTTAGGGATCC 96

RESULT 14

ABD00374/c
ID ABD00374 standard; DNA; 1245 BP.

XX ABD00374;

XX ABD00374;

XX 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polynucleotide seqid 6149.

XX Recombinant expression vector; transcription regulatory element;

KW

KW Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.

XX Klebsiella pneumoniae.

OS US6610836-B1.

PN 26-AUG-2003.

PD 27-JAN-2000; 2000US-00489039.

PF 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

PA Breton GL, Osborne M;

PI WPI; 2003-895346/82.

XX P-PSDB; ABO66803.

PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 6149; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention

XX Sequence 1245 BP; 229 A; 431 C; 380 G; 205 T; 0 U; 0 Other;

Query Match 5.8%; Score 95.6; DB 11; Length 1245;

Best Local Similarity 65.4%; Pred. No. 1.4e-08;

Matches 140; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 17 CTTCCGCGACCGGGCTACCGGGTGGCTGACGTACTCCGGCCATCCGCTGGCGACCGC 76

Db 475 CTTTGACGACCACTTTCTTGGCGGGGGCTGACCTACTCCGGCCATCCGCTGGCGATGGC 416

QY 77 CTGCGGGTCTGGACGATCAACCGGATGGAAGACGAAGCATGGTGGCCAAACGCTGCCGC 136

Db 415 GCGGATTTGCGCCACCATCGACCGGATGAAGAGGAGATGTGTTGAGAACCGCGCCTC 356

QY 137 CATCGCGACGAGGTGTCGACCGGGTCTGCGGATCTCGCGCCCGGACCGTTTCGGT 196

Db 355 TATCGGCAACGAGGTGTCGCGCCCGGTCTCGAGGCGCTGGCGGAGACCGCCATTAT 296

QY 197 CGGCGAAGTCCGCGGCTCGGCGTCTTCTGGCG 230

Db 295 CGGCGAGGTGCGGGTCCGCGGCTGTTCAGGCG 262

RESULT 15

ABD00219

ID ABD00219 standard; DNA; 1371 BP.

XX ABD00219;

XX 29-JUL-2004 (first entry)

DE Klebsiella pneumoniae polynucleotide seqid 5994.

XX Recombinant expression vector; transcription regulatory element;

KW Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.

OS Klebsiella pneumoniae.

XX US6610836-B1.

PN 26-AUG-2003.

XX 27-JAN-2000; 2000US-00489039.

XX 29-JAN-1999; 99US-0117747P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Breton GL, Osborne M;

XX WPI; 2003-895346/82.

DR P-PSDB; ABO66648.

XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for preparing a vaccine composition against Klebsiella pneumoniae.

XX Disclosure; SEQ ID NO 5994; 932pp; English.

XX The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention

XX Sequence 1371 BP; 245 A; 409 C; 462 G; 255 T; 0 U; 0 Other;

Query Match 5.8%; Score 95.6; DB 11; Length 1371;

Best Local Similarity 65.4%; Pred. No. 1.4e-08;

Matches 140; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 17 CTTCCGCGACCGGGCTACCGGGTGGCTGACGTACTCCGGCCATCCGCTGGCGACCGC 76

Db 942 CTTTGACGACCACTTTCTTGGCGGGGGCTGACCTACTCCGGCCATCCGCTGGCGATGGC 1001

QY 77 CTGCGGGTCTGGACGATCAACCGGATGGAAGACGAAGCATGGTGGCCAAACGCTGCCGC 136

Db 1002 GCGGATTTGCGCCACCATCGACCGGATGAAGAGGAGATGTGTTGAGAACCGCGCCTC 1061

QY 137 CATCGCGACGAGGTGTCGACCGGGTCTGCGGATCTCGCGCCCGGACCGTTTCGGT 196

Db 1062 TATCGGCAACGAGGTGTCGCGCCCGGTCTCGAGGCGCTGGCGGAGACCGCCATTAT 1121

QY 197 CGGCGAAGTCCGCGGCTCGGCGTCTTCTGGCG 230

Db 1122 CGGCGAGGTGCGGGTCCGCGGCTGTTCAGGCG 1155

Search completed: October 6, 2005, 20:46:31

Job time : 868 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 19:16:22 ; Search time 4974 Seconds
(without alignments)
12665.132 Million cell updates/sec

Title: US-10-607-752-115

Perfect score: 1655

Sequence: 1 gatctactactgaccttc.....atccaccatcaccatcactga 1655

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hcc.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87.6	5.3	1798	9	AG171124 Pan trogl
2	78.8	4.8	1772	9	CL508812 SAIL_802
3	78	4.7	1516	4	BG809984 mgct002xd
4	78	4.7	2332	9	AG363333 Mus muscu
5	77.8	4.7	1173	6	CB207639 AGENCOURT
6	76.8	4.6	2243	9	AG381986 Mus muscu
7	76.4	4.6	1538	9	AG030607 Pan trogl
8	76.4	4.6	1669	9	AG072737 Pan trogl
9	76.4	4.6	1821	9	CL090560 ISB1-17N1
10	75.8	4.6	1569	9	AG341503 Mus muscu
11	75.6	4.6	925	9	CNS0091P
12	75.6	4.6	1299	9	AG039481 Pan trogl
13	75.4	4.6	1247	9	AG035314 Pan trogl
14	74.8	4.5	1878	9	AG393083 Mus muscu
15	73.4	4.4	1569	9	AG341503 Mus muscu
16	73.2	4.4	937	9	AG080291 Pan trogl
17	73	4.4	925	9	CNS0091P
18	72.8	4.4	932	9	CNS0072Q
19	72.8	4.4	1516	4	BG809984 mgct002xd
20	72.6	4.4	940	7	CK404835 AUF Ifsnp
21	72.6	4.4	2243	9	AG381986 Mus muscu
22	72.4	4.4	1328	9	AG043615 Pan trogl
23	71.4	4.3	1045	5	BUI190119 AGENCOURT
24	71.2	4.3	992	9	AG057280 Pan trogl

25	71.2	4.3	1821	9	CL090560
26	71	4.3	1552	9	AG430101 Mus muscu
27	71	4.3	1798	9	AG171124 Pan trogl
28	70.8	4.3	932	9	CNS0072Q
29	70.8	4.3	1406	9	CG756569 P051-4-B0
30	70.4	4.3	1780	9	AG48243 Mus muscu
31	70.2	4.2	1421	8	BZ569488 pac82-164
32	70.2	4.2	1772	9	CL508812 SAIL_802
33	69.4	4.2	1137	4	BG809979 mgct002xd
34	69.4	4.2	1151	9	AG046212 Pan trogl
35	69.4	4.2	1280	9	CL470317 SAIL_140
36	69.4	4.2	1610	8	BZ569386 pac82-164
37	69.2	4.2	1971	5	BQ961185 AGENCOURT
38	69.2	4.2	1233	6	CA975828 AGENCOURT
39	69	4.2	997	9	AG057392 Pan trogl
40	68.8	4.2	1610	8	BZ569386 pac82-164
41	68.4	4.1	1126	9	AG064051 Pan trogl
42	68.4	4.1	1780	9	AG48243 Mus muscu
43	68.4	4.1	1878	9	AG393083 Mus muscu
44	68.4	4.1	1981	9	CL515231 SAIL_898
45	68	4.1	784	9	AG060328 Pan trogl

ALIGNMENTS

RESULT 1	AG171124/c	AG171124	Pan troglodytes DNA, clone: RP43-040F09.TU, genomic survey	1798 bp	DNA	linear	GSS 09-JAN-2002
LOCUS	AG171124	sequence.					
DEFINITION	AG171124	GI:16700802					
ACCESSION	AG171124	GI:16700802					
VERSION	AG171124.1						
KEYWORDS	GSS.						
SOURCE	Pan troglodytes (chimpanzee)						
ORGANISM	Pan troglodytes						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.						
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.						
TITLE	BAC end sequences of Library RPCI-43						
JOURNAL	Unpublished						
REFERENCE	2 (bases 1 to 1798)						
AUTHORS	Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.						
TITLE	Direct Submission						
JOURNAL	Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)						

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : ECORI

R.Site 2 : ECORI

source

Location/Qualifiers

1. 1798

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-040F09.TJ"

/sex="male"

/cell_type="lymphocytes"

/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 5.3%; Score 87.6; DB 9; Length 1798;

Best Local Similarity 41.1%; Pred. No. 1.1e-08; Matches 533; Conservative 0; Mismatches 750; Indels 13; Gaps 7;	
QY	21 GCCGACCGGCGTACCCGGTGTGCTGAGCTACTCCGGGCATCCGTGTGGCGACCGCTGC 80
Db	1691 GCGGCGGNGGCG 1632
QY	81 GCGGTCCGACGATCAACCGCATGGAAGACGAAGGATGTTGCC-AAAGTGTCCCGCAT 139
Db	1631 GCGCGNCCG 1572
QY	140 CGCGAGCAGGTGCTCGACCGGGTCTGCGCATCTCGCGCGCGCGCGCGCGCGCGCGCG 197
Db	1571 CG 1512
QY	198 GCGCAAGTCCGCGCGCTCGCGCTCTTCTGGCGCGGATCTGATCCAGAAAGCGGCGCGTCTG 257
Db	1511 GNGGCGGCGCGGNGGNGGCG 1452
QY	258 CGGTTGAGTCTCTCGGTGCCAGTGCCTGTCGACGACGTCGTCTCGCGCGTGTGATGCG 317
Db	1451 CGNGGCG 1392
QY	318 GCGCGGTAGGCTCTCGTCCACAACTCAGACCGTGCCTCGCGCGCGCGCGCGCGCGCG 377
Db	1391 GCGNCCCG 1332
QY	378 AGTTCCGCCCTGTCTCGCACCGCGCGAGGCGAGCCAGTTTCCGCTCCGGCGTTCGATCGGG 437
Db	1331 CGCGCGCGCGCG -CG 1273
QY	438 TTGCGTCCGTCGCGCAGACACAAGCATCCACGAGTTCGAGAACCGGTCCCCGACG 497
Db	1272 NGCGCGCNCNGCG 1213
QY	498 GTGCACATCTCCAGTCGATGAACG -CGCGAGCTCGGGAGCTTCGCGCGCGAGCAGCAC 556
Db	1212 GCGGGCGNNGCG 1153
QY	557 GTTGTTCAGATGGCAGTCGCGTCATGATCCCGGGTTCCGGCTCTGTCGGCGCTGCGCGA 616
Db	1152 NGCGNNGCG 1093
QY	617 GTCCAGCATCTCGCGAGACATGACACGACGCGGAGACGATCGGGCGCGGATCTGATCA 676
Db	1092 GNGNCGCGCGCGCGNNGCG 1034
QY	677 GCTCGGGAGCGCGGTGCCAGCAACGCCAGCTGTGGAGCACCGAGACCGCGCGCATGT 736
Db	1033 CGCGGCG 974
QY	737 GCGCGCGCAGCAGCGCCAGCTGTGACCCCGCGGGACCGGGCCCGCGGACCGCGTCGG 796
Db	973 CGCGGNGGCGCGGGCGCGCGNNGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 914
QY	797 AGTCGACCCCGCGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 856
Db	913 NNGCG 854
QY	857 TCGGCAGGCATCAGAACAGTAAAGCGGTTCGGTTGATTCAAATGTCGTGTCAGCAGG 916
Db	853 CGCGGGGCG 794
QY	917 CATCCGATGCGCAACACCGACCGCAGCAGTTCGCAA---TCTGTCTCGCGACCTTGGC 973
Db	793 CGGCG 734
QY	974 GTACCGGGCGTCTGTGCTCGGMAACCGCGCGGGATGTTCGCGCGCGCGCGCGCGCG 1029
Db	733 CG 674
QY	1030 CGGCTCTCTCATGGCGGTTCGTTCAGTCTGTCGCGGTGGTGTCTTCGCAACGGCGC 1089
Db	673 CG 614
QY	1090 CGCGCGCGCGTCTGTCGTCCGATACGGGATCTATCAGCAGTAGCGCGTCCAGCGGTAC 1149
Db	613 CG 554
QY	1150 TCTTCGCGCCAGAACAGCGGTGCGTCCGCGCGAGACAGCGGTCTCTGCGCCAGATAC 1209
Db	553 GCGNCCCG 494
QY	1210 ACCCAGCGGTGCGCGCATGTCTCAGATCTGTCGCGCAGCGCGCGCGCGCGCGCG 1269
Db	493 CG 434
QY	1270 GATCTATCTGCGCGGTGTGTCGCGGAGGACGAGGCGCG 1305
Db	433 CG 398
RESULT 2	
CL508812/c	
LOCUS	
DEFINITION	
SAIL 802_H02.v1 SAIL Collection Arabidopsis thaliana genomic clone	
SAIL 802_H02.v1, genomic survey sequence.	
CL508812.1 GI:46006132	
GSS.	
Arabidopsis thaliana (thale cress)	
Arabidopsis thaliana	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.	
1 (bases 1 to 1772)	
Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,	
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,	
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,	
Mittel,T., Katagiri,P., Glazebrook,J., Law,M. and Goff,S.A.	
A high-throughput Arabidopsis reverse genetics system	
Plant Cell 14 (12), 2985-2994 (2002)	
22356987	
PUBMED	
12468722	
COMMENT	
Contact: Sessions A	
Applied Trait Genetics	
Syngenta Biotechnology Inc.	
3054 Cornwalls Rd., Research Triangle Park, NC 27709, USA	
Email: allen.sessions@syngenta.com	
ABRC Stock Number CS835878; T-DNA left border flanking sequences of	
Syngenta Arabidopsis Insertion Library (SAIL) lines are available	
through the Arabidopsis Biological Resource Center (ABRC).	
Sequences represent a pool of amplified genomic regions and not	
single contiguous sequences.	
Class: TDNA tagged.	
FEATURES	
source	
1..1772	
Location/Qualifiers	
/organism="Arabidopsis thaliana"	
/mol_type="genomic DNA"	
/ecotype="Columbia"	
/db_xref="taxon:3702"	
/clone_lib="SAIL 802_H02.v1"	
/clone_lib="SAIL Collection"	
/note="T-DNA left border sequences were isolated using a	
modified TAIL-PCR strategy"	
ORIGIN	
Query Match 4.8%; Score 78.8; DB 9; Length 1772;	
Best Local Similarity 44.0%; Pred. No. 9.4e-07;	
Matches 532; Conservative 0; Mismatches 669; Indels 9; Gaps 5;	
QY	64 CGTGTGCGACCGCTCGCGGTTCGCGACGATCAACCGCATGGAAGACGAGCATGCTGG 123
Db	1273 CG 1214
QY	124 CCACGCTGCGCGCATCGCGAGCAGGTCTCGGACCGGGGTCTGCGCGATCTCGCGCGCC 183

QY 442 GTCCGTCCGCCAGACACACAGATCCACCCGAGCTCGAGCAACCGGTCCCGAGC--GT 499
 Db 1172 GCGCGCGNGNNGNCCGCGCGCGGCGNCGNCGNGGCGCGCGCGCGCGCGCGCGCG 1113
 QY 500 GCACATCTCCAGTCTCATGAACCGCCGAGCTCGGGACGTCGCGCGCGAGCAGCAGT 559
 Db 1112 GNCNCCG 1053
 QY 560 GTTCAGATGGCAGTCCCGTGTGATGATCCCGGTTGCGGTCGTGCGGCTCGCGAGTTC 619
 Db 1052 CG 994
 QY 620 CAGCCAGTGGCGGACACATGACACGACGGAACGACTCGCGCGCGGAGATCTGATCAGT 679
 Db 993 CG 934
 Db 680 CGCGGAGCGCGGTGCGCAGACCGCAGCGTGTGGAGACACCGAGACCGCGCGGATGTGCC 739
 Db 933 CGCGGCG 874
 QY 740 CGCGCAGCAGCGCCAGCGTGTGACCCCGCGGAGACCGGCGCGCGCGCGCGCGCG 799
 Db 873 CGCGGCG 814
 QY 800 CGACCCCG 859
 Db 813 CG 754
 QY 860 GCAGGCGATCAGCAACAGTAAAGCG--GTGTTCCGCTTGAATCCAAATGCTGTGTCAGCAGGCA 918
 Db 753 NGGGGCG 694
 QY 919 TCAGTATGCCGAAACACGACACGAGAGAGTGTGCAATCTGTCTGCGACACCTTGCGTAC 978
 Db 693 GCNCG 634
 QY 979 GCGCGCTGTGCTCGCAACCGCGCGGATGTGCGCGCGCGCGCGCGCGCGCGCTTC 1038
 Db 633 GCGCNGGCG 574
 QY 1039 CATGGCGCGTTCCTTCACTGCTCGTCCGCTGCTGTCTTTCGAAACCGCGCGCGCG 1098
 Db 573 NGCG 514
 QY 1099 GTCGTCTCGTCCGATAGAGATCTATCAGCAGATGAGCGTTCAGCGCTACTTTCGCC 1158
 Db 513 CCG 454
 QY 1159 CAGAACAGCGGTGCGTCCGCGCGCAGACACAGCGGTCTTTCGCGCAGATACACCGAGG 1218
 Db 453 GCNCG 394
 QY 1219 GTGCGCGCGATGTCAGATCGTGGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1278
 Db 393 GNGCG 334
 QY 1279 CGCGGCTGTGCGGAGAGACGAGGCGG 1305
 Db 333 CGCGGCG 307

RESULT 4
 AG363333
 LOCUS Mus musculus molossinus DNA, clone:MSMg01-165A22.TJ, genomic survey
 DEFINITION
 AG363333
 sequence.
 AG363333
 VERSION
 AG363333.1 GI:47974538
 GSS.
 KEYWORDS Mus musculus molossinus
 SOURCE Mus musculus molossinus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 BAC end Sequences of Library MSMg01
 2 (bases 1 to 2332)
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Direct Submission
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
 1-22 Suehiro-chou,Tsuri-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@psc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC
 library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
 Tsukuba Institute, Bio Resource Center.
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp
 PRIMERS
 Sequencing : TJ
 LIBRARY : pBACE3.6
 Vector : EcoRI
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.

FEATURES
 source
 1..2332
 Location/Qualifiers
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-165A22.TJ"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 4.7%; Score 78; DB 9; Length 2332;
 Best Local Similarity 44.2%; Pred. No. 1.4e-06;
 Matches 572; Conservative 0; Mismatches 695; Indels 27; Gaps 5;
 QY 21 GCCGACCGCGGCGTACCCGCGTGCCTGACGTACTCCGCGCATCCCGTGGCGACCGCGTGC 80
 Db 947 GCG 1006
 QY 81 GCGGTGCGGACGATCAACCGGATGGAAGCAAGCAAGCATGTGGCCAGCTGCCCGCATC 140
 Db 1007 CGCGGCG 1066
 QY 141 GCGGACGAGGTCTCTCGGACCGGGTCTGCGCGCATCTCGCGCGCGCGCGCGCGCGCG 200
 Db 1067 CCGG-GCGGCG 1125
 QY 201 GAAGTCCGCGGCTCGCGGTCTTTCGCGCGGATCTGATTCAGAACGCGGCGCGGTTCGCG 260
 Db 1126 CCG 1185
 QY 261 GTTGAGTCTCTCGGTCCCGTGCAGCGGATGCGCGCGCGCGCGCGCGCGCGCGCGCG 320
 Db 1186 CCG 1245
 QY 321 GCGGTAGGCGTCTCTCGGTCCACAAAGTCAGCAACCGTGCCTCGCGCGCGGATGGATCTAT 380
 Db 1246 CCGCGGTGCG 1305
 QY 381 TCGGCGCTGTGCGCAGCG 440
 Db 1306 GCGGCG 1365
 QY 441 GGTCTGTC--CGGCCAGCACACCGATCCACCGAGGTTCGAGCAACGCGGTCCCCACCG 498
 Db 1366 CCG 1425

Qy 964 CGACCTTGGGCTCACGGCGGTCTGTGGCTCCGCAACCCCGCGCGATGTGCGCGCGCG 1023
Db 1126 CCGGCGGGGCGCGGGCCCCCGCGCGCCCCCGGGCGCGCGCGCGCGCGCGCGCG 1067
Qy 1024 CTGCGGCGGGCTCTCCATGGCCGGTGTGTTAGTCTGCTGTGCTGGTGGCTGTCTCGGAA 1083
Db 1066 CGGCGGCGGGCGCGGGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1007
Qy 1084 CGGCGCGCGCGCGCGCGCGTCTGTC 1105
Db 1006 CCGGCGGGCG 985

RESULT 7
AG030607 1538 bp DNA linear GSS 01-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-003A18.F, genomic survey sequence.
AG030607
ACCESSION
VERSION AG030607.1 GI:16557480
KEYWORDS
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1538)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Ageo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanzee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB. This BAC end
clone was generated during the R&D process and may have higher chance of
PRIMERS

Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. 1538
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-003A18.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

FEATURES
source

Query Match 4.6%; Score 76.4; DB 9; Length 1538;
Best Local Similarity 38.8%; Pred. No. 3.1e-06;
Matches 426; Conservative 0; Mismatches 666; Indels 5; Gaps 2;
Qy 128 CGTGTCCGATCGGCGAGAGGTGCTCGGACCGGGGTCTGGCGCATCTCGCGCGCGCGCA 187
Db 338 CGCGCGCGGNNCGCCCG 397
Qy 188 CCGTTCGGTCCGGAGTCCCGCGCGCTCTCTTCTGGCGGGATCTGATCCAGAACG 247
Db 398 CCG 457
Qy 248 GCGCGGTCTGGGGTTGAGGTCTCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
Db 458 CCG 517

ORIGIN
Query Match 4.6%; Score 76.4; DB 9; Length 1538;
Best Local Similarity 38.8%; Pred. No. 3.1e-06;
Matches 426; Conservative 0; Mismatches 666; Indels 5; Gaps 2;

Qy 128 CGTGTCCGATCGGCGAGAGGTGCTCGGACCGGGGTCTGGCGCATCTCGCGCGCGCGCA 187
Db 338 CGCGCGCGGNNCGCCCG 397
Qy 188 CCGTTCGGTCCGGAGTCCCGCGCGCTCTCTTCTGGCGGGATCTGATCCAGAACG 247
Db 398 CCG 457
Qy 248 GCGCGGTCTGGGGTTGAGGTCTCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
Db 458 CCG 517

RESULT 8
AG072737/c
LOCUS Pan troglodytes DNA, clone: PTB-064F05.F, genomic survey sequence.
AG072737
ACCESSION
VERSION AG072737.1 GI:16624539
KEYWORDS GSS.

Qy 308 TGTGTATGTGCGCGCGCGTCTAGGCGTCTCTCGGTCCACAAACGTCTAGCACCTGTCCTCGGCGGCA 367
Db 518 CCGGCG 577
Qy 368 TGTGTATATAGTTCTGGGCTCTGTGCG-CAGCCCGCGGAGGCGAGCAGTTCGCTCTCGG 426
Db 578 NGGCGGCG 637
Qy 427 CGTGTATCGGTTGGGTCTCGTCCGGCCAGACACACAGCATCCACCCGAGAGTCTCAGCAACG 486
Db 638 CG 697
Qy 487 GGTCTCCCGAGCGGTGCACATCTCTCAGTTCGATGAACCCCGCGAGCTCTGGGAGACCTCGCGCG 546
Db 698 CCG 757
Qy 547 GCGAGGACAGTTGTTTCAGATGGCAGTCTCGCGTGCATGATCTCCGGGTTTGGGCTCTGTCGG 606
Db 758 GGCNCAGNCNCG 817
Qy 607 GCCTGCGCGAGTCCAGCCAGTCTGGCGAGCAGATGACACCGAGCGGAAACGACTCTCGGCGCGCG 666
Db 818 GCG 877
Qy 667 GATCTCTGATCAGTCTCGGCGAGCGCGGTTGCCAGCAACCGCAGCGTGGGAAAGCACCCGAGACC 726
Db 878 GCGCGGNCNCG 933
Qy 727 GCGCGGATGTGCGCGCGAGCG 786
Db 934 CG 993
Qy 787 ACCCGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 846
Db 994 CG 1053
Qy 847 ATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 906
Db 1054 GCG 1113
Qy 907 TGTCTAGGAGGATCTCGATGCGCGAAACCGAGCACCGGAGAGTCTGATCTGATCTGATCTGATCT 966
Db 1114 CG 1173
Qy 967 CCCTGGGCTCACCGGCGGTCTGCTCTCGGCAACCCCGCGCGAGTCTGCGCGCGCGCGCTG 1026
Db 1174 NCCCCG 1233
Qy 1027 CGCGCGCGCTCTCCATGCGCGCGTTCGTTTCTAGTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1086
Db 1234 GCGCGGCG 1293
Qy 1087 GCG 1146
Db 1294 GCG 1353
Qy 1147 TACTCTTCCGCGCGAGAACAGCGGTCTGCTCTGCGCGCGAGACAGCGGTCTGCTGCGCGCGCA 1206
Db 1354 CCACGCGGCG 1413
Qy 1207 TACACCGCGCGGTGGC 1223
Db 1414 GCG 1430

RESULT 8
AG072737/c
LOCUS Pan troglodytes DNA, clone: PTB-064F05.F, genomic survey sequence.
AG072737
ACCESSION
VERSION AG072737.1 GI:16624539
KEYWORDS GSS.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: October 6, 2005, 20:14:37 ; Search time 1112 Seconds
(without alignments)
10365.839 Million cell updates/sec

Title: US-10-607-752-115
Perfect score: 1655
Sequence: 1 gatcatctactgcaccttc.....atcaccatcaccatcactga 1655

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues
Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/US06_PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/1/pubpna/US07_PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1655	100.0	1655	18	US-10-607-752-115
2	1655	100.0	1749	14	US-10-100-607-58
3	1655	100.0	1749	14	US-10-607-752-58
4	1623	98.1	1623	14	US-10-100-607-89
5	1623	98.1	1623	14	US-10-607-752-89
6	1413	85.4	1413	14	US-10-100-607-88
7	1413	85.4	1413	18	US-10-607-752-88
					Sequence 115, App
					Sequence 58, Appl
					Sequence 58, Appl
					Sequence 89, Appl
					Sequence 89, Appl
					Sequence 88, Appl
					Sequence 88, Appl

8	1247	75.3	1263	14	US-10-100-607-87	Sequence 87, Appl
9	1247	75.3	1263	18	US-10-607-752-87	Sequence 87, Appl
10	1116	67.4	1116	14	US-10-100-607-86	Sequence 86, Appl
11	1116	67.4	1116	18	US-10-607-752-86	Sequence 86, Appl
12	1011.4	61.1	1749	14	US-10-100-607-56	Sequence 56, Appl
13	1011.4	61.1	1749	18	US-10-607-752-56	Sequence 56, Appl
14	843	50.9	843	14	US-10-100-607-85	Sequence 85, Appl
15	843	50.9	843	18	US-10-607-752-85	Sequence 85, Appl
16	740.2	44.7	1749	14	US-10-100-607-57	Sequence 57, Appl
17	740.2	44.7	1749	18	US-10-607-752-57	Sequence 57, Appl
18	660	39.9	660	14	US-10-100-607-84	Sequence 84, Appl
19	660	39.9	660	18	US-10-607-752-84	Sequence 84, Appl
20	363	21.9	363	14	US-10-100-607-83	Sequence 83, Appl
21	363	21.9	363	18	US-10-607-752-83	Sequence 83, Appl
22	291	17.6	291	14	US-10-100-607-15	Sequence 15, Appl
23	291	17.6	291	18	US-10-607-752-15	Sequence 15, Appl
24	261	15.8	261	14	US-10-100-607-18	Sequence 18, Appl
25	261	15.8	261	18	US-10-607-752-18	Sequence 18, Appl
26	226	13.7	697	14	US-10-100-607-14	Sequence 14, Appl
27	226	13.7	697	18	US-10-607-752-14	Sequence 14, Appl
28	225	13.6	225	14	US-10-100-607-82	Sequence 82, Appl
29	225	13.6	225	18	US-10-607-752-82	Sequence 82, Appl
30	210	12.7	210	14	US-10-100-607-13	Sequence 13, Appl
31	210	12.7	210	18	US-10-607-752-13	Sequence 13, Appl
32	177	10.7	177	14	US-10-100-607-21	Sequence 21, Appl
33	177	10.7	177	18	US-10-607-752-21	Sequence 21, Appl
34	147	8.9	147	14	US-10-100-607-16	Sequence 16, Appl
35	147	8.9	147	18	US-10-607-752-16	Sequence 16, Appl
36	138	8.3	138	14	US-10-100-607-17	Sequence 17, Appl
37	138	8.3	138	18	US-10-607-752-17	Sequence 17, Appl
38	132.4	8.0	1353	15	US-10-156-761-4535	Sequence 4535, Ap
39	132.4	8.0	9025608	15	US-10-156-761-4535	Sequence 1, Appl
40	132	8.0	132	14	US-10-100-607-20	Sequence 20, Appl
41	132	8.0	132	18	US-10-607-752-20	Sequence 20, Appl
42	114	6.9	114	14	US-10-100-607-11	Sequence 11, Appl
43	114	6.9	114	18	US-10-607-752-11	Sequence 11, Appl
44	96	5.8	96	14	US-10-100-607-9	Sequence 9, Appl
45	96	5.8	96	18	US-10-607-752-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-10-607-752-115
; Sequence 115, Application US/10607752
; Publication No. US2004007224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042C3
; CURRENT APPLICATION NUMBER: US/10/607,752
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-607-752-115

Query Match 100.0%; Score 1655; DB 18; Length 1655;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCTATCTACTCGACCTTCCGCGACGCGGCGTACCCGGGTGGCCTTGAGCTACTCCGGCC 60
DB |||||
1 GATCTATCTACTCGACCTTCCGCGACGCGGCGTACCCGGGTGGCCTTGAGCTACTCCGGCC 60
QY 61 ATCCGCTGGGCGACCGCTTCGCGGCTCGCACGATCAACGCGATGGAAGAGCAAGGCATGG 120
DB |||||
61 ATCCGCTGGGCGACCGCTTCGCGGCTCGCACGATCAACGCGATGGAAGAGCAAGGCATGG 120
QY 121 TGGCCAAACGCTGCCCGCATCGGCGACGAGTGCTCGGAACCGGCTTCGCGGATCTCGCGG 180
DB |||||
121 TGGCCAAACGCTGCCCGCATCGGCGACGAGTGCTCGGAACCGGCTTCGCGGATCTCGCGG 180
QY 181 CCGGCGACCTTCGCTCGGCGAAGTTCGGGCGCTTCGGGCTCTTCGGGCGGATCTGATC 240
DB |||||
181 CCGGCGACCTTCGCTCGGCGAAGTTCGGGCGCTTCGGGCTCTTCGGGCGGATCTGATC 240
241 CAGAACGGGCGGCTTCGCGGCTTCGAGTCTCGGTGCCAGATGCCGTCGACGCGACGCTCG 300
DB |||||
241 CAGAACGGGCGGCTTCGCGGCTTCGAGTCTCGGTGCCAGATGCCGTCGACGCGACGCTCG 300
QY 301 TCGCGCTGCTGATCGGCGCGCGTTCGAGGCTCTCGGTCCAAACGTCGACGACCGTGC 360
DB |||||
301 TCGCGCTGCTGATCGGCGCGCGTTCGAGGCTCTCGGTCCAAACGTCGACGACCGTGC 360
QY 361 GGGCGGATGATCTATCAGTTCCGGCTTCGTCGCGAGCGCGCGGCGAGCGAGTTCG 420
DB |||||
361 GGGCGGATGATCTATCAGTTCCGGCTTCGTCGCGAGCGCGCGGCGAGCGAGTTCG 420
QY 421 CTCGGCGTCGATCGGGCTTCGGCTTCGGTCGGCGCAGACACGACATCCACCCGAGTCCA 480
DB |||||
421 CTCGGCGTCGATCGGGCTTCGGCTTCGGTCGGCGCAGACACGACATCCACCCGAGTCCA 480
QY 481 GCAACGGGTCCTCCGACGGTGCACATCTCCAGTTCGATGAACGCGCGGAGCTCGGGGACGT 540
DB |||||
481 GCAACGGGTCCTCCGACGGTGCACATCTCCAGTTCGATGAACGCGCGGAGCTCGGGGACGT 540
QY 541 CGGCGCGACAGCAGCTTCGTCGATGGCAGTTCGGCTGCATGATCCCGGCTTCGGCGCT 600
DB |||||
541 CGGCGCGACAGCAGCTTCGTCGATGGCAGTTCGGCTGCATGATCCCGGCTTCGGCGCT 600
QY 601 CGTCGGGCTTCGCGAGTCCAGCGAGTCCGCGGAGCAGATCCAGCGAGGAAACGACTCGG 660
DB |||||
601 CGTCGGGCTTCGCGAGTCCAGCGAGTCCGCGGAGCAGATCCAGCGAGGAAACGACTCGG 660
661 GCGCGGATCTGATCAGCTCGGCGAGCGCGGTGCGGAGCAACGCGAGCTGGGAGGAC 720
DB |||||
661 GCGCGGATCTGATCAGCTCGGCGAGCGCGGTGCGGAGCAACGCGAGCTGGGAGGAC 720
QY 721 GAGACCGCGGATGTCGCCGCGCAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 780
DB |||||
721 GAGACCGCGGCGATGTCGCCGCGCAGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 781 CCGCGGACCGGCTCGGAGTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
DB |||||
781 CCGCGGACCGGCTCGGAGTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 841 CACGGGATGATCTGATCGGCGAGCATCAAGAACTGAGCGGTTCGGGTGGAATCCA 900
DB |||||
841 CACGGGATGATCTGATCGGCGAGCATCAAGAACTGAGCGGTTCGGGTGGAATCCA 900
QY 901 ATGTGCTGTACGAGGATCCGATGCGGAACACCGGACCGCGAGCTCGCAATCTGTC 960
DB |||||
901 ATGTGCTGTACGAGGATCCGATGCGGAACACCGGACCGCGAGCTCGCAATCTGTC 960
QY 961 TCGCGACCTTCGCTCGCGGCGCTTCGTCGCGAACCAGCGCGGCGATGTCGCGCGG 1020
DB |||||
961 TCGCGACCTTCGCTCGCGGCGCTTCGTCGCGAACCAGCGCGGCGATGTCGCGCGG 1020
QY 1021 CCGCTCGGCGCGGCTTCATGCGCGGCTTCGTCGAGTTCGTCGCGGCTTCGCTTCG 1080
DB |||||
1021 CCGCTCGGCGCGGCTTCATGCGCGGCTTCGTCGAGTTCGTCGCGGCTTCGCTTCG 1080

QY 1081 GAAACGGGCGCGCGCGCTTCGTCGCGATACGCGATCTATCACGAGGTAGGCGGTC 1140
DB |||||
1081 GAAACGGGCGCGCGCGCTTCGTCGCGATACGCGATCTATCACGAGGTAGGCGGTC 1140
QY 1141 CAGCGGTACTCTTCGCGCGCGAGAAACGCGGTTCGCGCGAGACAGCGGTCTCTGCC 1200
DB |||||
1141 CAGCGGTACTCTTCGCGCGCGAGAAACGCGGTTCGCGCGAGACAGCGGTCTCTGCC 1200
QY 1201 GCCAGATACCCAGCGGCTTCGCGCGATGTCAGATCGTGGCCAGCGCGCGGACG 1260
DB |||||
1201 GCCAGATACCCAGCGGCTTCGCGCGATGTCAGATCGTGGCCAGCGCGCGGACG 1260
QY 1261 TGGAGATCGGATCTATCGCGCGCTTCGCGGAGAGACGAGCGGTAGCGGCTTGCACT 1320
DB |||||
1261 TGGAGATCGGATCTATCGCGCGCTTCGCGGAGAGACGAGCGGTAGCGGCTTGCACT 1320
QY 1321 AGCTCGCGCGGTTGCGGAGAGAGACTACATCGACGAGGCTTCGCGCAATCGGCG 1380
DB |||||
1321 AGCTCGCGCGGTTGCGGAGAGAGAGACTACATCGACGAGGCTTCGCGCAATCGGCG 1380
QY 1381 CGTATCTGCCAGCTGAGTTCCGCTTCGTCGAGTCTATCGCGCGACCGGCTTCGCG 1440
DB |||||
1381 CGTATCTGCCAGCTGAGTTCCGCTTCGTCGAGTCTATCGCGCGACCGGCTTCGCG 1440
QY 1441 CCGGCGACCGCTGAGTTCGTCAGTACCCGAGCTCTTGAGAGCTAAGGCAATGGG 1500
DB |||||
1441 CCGGCGACCGCTGAGTTCGTCAGTACCCGAGCTCTTGAGAGCTAAGGCAATGGG 1500
QY 1501 AAGATCTTGAGACTTCCATCAATAGAGAAAGCATCGGCTAGGAGATCGTAGCGG 1560
DB |||||
1501 AAGATCTTGAGACTTCCATCAATAGAGAAAGCATCGGCTAGGAGATCGTAGCGG 1560
QY 1561 GCGCGGCTTCGAGTGAATTTGGCGAGGCAATCCCATCGCGCGAGCGCGCGAGCGG 1620
DB |||||
1561 GCGCGGCTTCGAGTGAATTTGGCGAGGCAATCCCATCGCGCGAGCGCGAGCGG 1620
QY 1621 AAATCCACGAGTCCCATCAACCATCACTCACTGA 1655
DB |||||
1621 AAATCCACGAGTCCCATCAACCATCACTCACTGA 1655

RESULT 2

US-10-100-679-58
; Sequence 58, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder.
; FILE REFERENCE: 11000.1042C2
; CURRENT APPLICATION NUMBER: US/10/100,679
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-100-679-58

Query Match 100.0%; Score 1655; DB 14; Length 1749;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATCTATCTACTCGACCTTCGCGCGAGCGGCGGTACCCGGGTGGCCTTGAGCTACTCCGGCC 60

Qy	1206	ATACACCCAGCGGCTGGCCGGCATGTCCAGATCGTGC	CCAGCGCGCGCGACCGTGGAG	1266
Db	1201	ATACACCCAGCGGCTGGCCGGCATGTCCAGATCGTGC	CCAGCGCGCGCGACCGTGGAG	1260
Qy	1266	ATCGGATCTATCCGCGGGCTGTGCGGGAAGACGAGG	CCGTAGCCGGTGTGCACTACGTC	1325
Db	1261	ATCGGATCTATCCGCGGGCTGTGCGGGAAGACGAGG	CCGTAGCCGGTGTGCACTACGTC	1320
Qy	1326	GCCTCCGGTTGGCAGAGAAGACGAGCTACATCGACCG	AGCCTTGGCGCAACATCGGGCCGTAT	1385
Db	1321	GCCTCCGGTTGGCAGAGAAGACGAGCTACATCGACCG	AGCCTTGGCGCAACATCGGGCCGTAT	1380
Qy	1386	CTGCCAGCTCAGGTTCCCGCTCTCTGTCGGATCTAT	CGCCGCCACCGGCGCCCGTCCCGGC	1445
Db	1381	CTGCCAGCTCAGGTTCCCGCTCTCTGTCGGATCTAT	CGCCGCCACCGGCGCCCGTCCCGGC	1440
Qy	1446	ACCGCTGGATCGTTCGTTCAGTACCCGGAAGCTCTT	GAGAGCTTAAGGCCAATTTGGGAAGAT	1505
Db	1441	ACCGCTGGATCGTTCGTTCAGTACCCGGAAGCTCTT	GAGAGCTTAAGGCCAATTTGGGAAGAT	1500
Qy	1506	ACTTGGACCTTCCCATCAATAGAGGAAAAGCATCGCC	CTAGGGATCCGTAGCGGGCCCG	1565
Db	1501	ACTTGGACCTTCCCATCAATAGAGGAAAAGCATCGCC	CTAGGGATCCGTAGCGGGCCCG	1560
Qy	1566	GTGTTTTCGAGTGAACCTTGGGCAGGGCAATCCCAT	TCGCGCAGCCCGCAGCGGAAATC	1625
Db	1561	GTGTTTTCGAGTGAACCTTGGGCAGGGCAATCCCAT	TCGCGCAGCCCGCAGCGGAAATC	1620
Qy	1626	CAC	1628	
Db	1621	CAC	1623	

RESULT 5

```

US-10-607-752-89
; Sequence 89, Application US/10607752
; Publication No. US2004007224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment
; TITLE OF INVENTION: and Methods for Their
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-607-752-89

```

Query Match	98.1%	Score 1623;	DB 18;	Length 1623;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1623. Conservative	0;	Mismatches	0;	Indels 0;
Matches 1623. Conservative	0;	Mismatches	0;	Gaps 0;

Qy	6	ATCTACTCGACGCTTTCCGCCGACCGGGCGTACCCGGGTGGCTTGACGCTACTCCGGGCATCCG	65
Db	1	ATCTACTCGACGCTTTCCGCCGACCGGGCGTACCCGGGTGGCTTGACGCTACTCCGGGCATCCG	60
Qy	66	CTGGCGACCGGCTTGCGCGGTCGCGACGATCAACCGGATGGGAAGACGAAGGCATGTGGCC	125
Db	61	CTGGCGACCGGCTTGCGCGGTCGCGACGATCAACCGGATGGGAAGACGAAGGCATGTGGCC	120
Qy	126	AACGTCGCCGGATCCGGCGACGAGTGTCTCGGACCGGGTCTTGGCGGATCTCGCCGCCCGG	185
Db	121	AACGTCGCCGGATCCGGCGACGAGTGTCTCGGACCGGGTCTTGGCGGATCTCGCCGCCCGG	180

QY	126	AACGCTGCCGCATCTCGCGAGCAGAGTGTCTCGACCGGGTCTCGCGCATCTCGCGCCCGCGG	185
DB	121	AACGCTGCCCGCATCGCGCAGCAGAGTGTCTCGACCGGGTCTCGCGCATCTCGCGCCCGCGG	180
QY	186	CACCGTTCCGTCGCGCGAAGTCTCGCGCCCTCGGCGTCTTCTGGGCGGGATCTGATCAGAA	245
DB	181	CACCGTTCCGTCGCGCGAAGTCTCGCGCCCTCGGCGTCTTCTGGGCGGGATCTGATCAGAA	240
QY	246	CGGGCCGGTCTCGGGGTTGAGGTCTCTCGTGCCTCGTGCAGTGCCTGCGGAGCGCATCTCGGC	305
DB	241	CGGGCCGGTCTCGGGGTTGAGGTCTCTCGTGCCTCGTGCAGTGCCTGCGGAGCGCATCTCGGC	300
QY	306	GCTGTGTGATCGCGCCGCGTGTGAGCGTCTCTCGGTCCAAACAGTCAGCACCGTGCCTCGGCGG	365
DB	301	GCTGTGTGATCGCGCCGCGTGTGAGCGTCTCTCGGTCCAAACAGTCAGCACCGTGCCTCGGCGG	360
QY	366	GATGGATCTATCAGTTTCGGCCCTGTGTGCGCAGCCCGCGAGGGCAGCCAGTTCGGCTCCG	425
DB	361	GATGGATCTATCAGTTTCGGCCCTGTGTGCGCAGCCCGCGAGGGCAGCCAGTTCGGCTCCG	420
QY	426	GCCTCGATCGGGTTGGGTCGTCGCGCCAGCACACAGCATCCACCCGAGGTTCGAGCAAC	485
DB	421	GCCTCGATCGGGTTGGGTCGTCGCGCCAGCACACAGCATCCACCCGAGGTTCGAGCAAC	480
QY	486	GGGTCCCGCAGCGGTGCACATCTCCAGTCGATGAACCGCCGAGCTCGGGAGCGTCCGCG	545
DB	481	GGGTCCCGCAGCGGTGCACATCTCCAGTCGATGAACCGCCGAGCTCGGGAGCGTCCGCG	540
QY	546	CGCAGCAGCATGTTGTTTCAGATGGCAGTTCGCGCTGCATGATCCCGGGTTCGGGTCGTCG	605
DB	541	CGCAGCAGCATGTTGTTTCAGATGGCAGTTCGCGCTGCATGATCCCGGGTTCGGGTCGTCG	600
QY	606	GGCTCGCGCAGTCCAGCCAGTTCGGCGAGCACATGCACCGAGGAAACGACTCGGCGCGG	665
DB	601	GGCTCGCGCAGTCCAGCCAGTTCGGCGAGCACATGCACCGAGGAAACGACTCGGCGCGG	660
QY	666	GGATCTCATCAGCTTCGGGAGCCGGGTGCCAGCAACCGCAGCGTGGGAAAGCACCGAGAC	725
DB	661	GGATCTCATCAGCTTCGGGAGCCGGGTGCCAGCAACCGCAGCGTGGGAAAGCACCGAGAC	720
QY	726	CGGGCCGATGTCGGCGCAGCAGCGCCAGCCGTCAGTGCACCCCGGAGCCCGGCCCGCGG	785
DB	721	CGGGCCGATGTCGGCGCAGCAGCGCCAGCCGTCAGTGCACCCCGGAGCCCGGCCCGCGG	780
QY	786	GACCGCTTCGAGTTCGACCCCGCGCCACCGCCGCGCGCTGGTCAGCATCAGCAACCG	845
DB	781	GACCGCTTCGAGTTCGACCCCGCGCCACCGCCGCGCGCTGGTCAGCATCAGCAACCG	840
QY	846	GATGGATCTGATTCGGCAGGCTACAGAACAGTAGCGGTGTTCCGGTTGAAATCCAAATG	905
DB	841	GATGGATCTGATTCGGCAGGCTACAGAACAGTAGCGGTGTTCCGGTTGAAATCCAAATG	900
QY	906	CTGTTCAGCAGGCATCTCGATGCCGAACACCGACACCGCAGCAGTCGCAATCTGTCTCGCG	965
DB	901	CTGTTCAGCAGGCATCTCGATGCCGAACACCGACACCGCAGCAGTCGCAATCTGTCTCGCG	960
QY	966	ACCTTGGCGTCAACCGCGGTCGTGGCTCCGCAACCCCGCGGCGATGTCGCGCGCGCGCT	1025
DB	961	ACCTTGGCGTCAACCGCGGTCGTGGCTCCGCAACCCCGCGGCGATGTCGCGCGCGCGCT	1020
QY	1026	CGGGCCGCTCTCCATGGCCGGTTTCGTTTCAGTCGCTCGTCCGGTGGCTGTTCTCGCAACG	1085
DB	1021	CGGGCCGCTCTCCATGGCCGGTTTCGTTTCAGTCGCTCGTCCGGTGGCTGTTCTCGCAACG	1080
QY	1086	GGCCCGCGCCCGCTCGTCCGATACGGGAATCTATCAGCAGGTAGGCGGTCCAGCC	1145
DB	1081	GGCCCGCGCCCGCTCGTCCGATACGGGAATCTATCAGCAGGTAGGCGGTCCAGCC	1140
QY	1146	GTACTTTTCGCCCCAGAAACAGCGGTTCGTCGCGCGCAGACAGCGGTCTTCGCGCGCAG	1205
DB	1141	GTACTTTTCGCCCCAGAAACAGCGGTTCGTCGCGCGCAGACAGCGGTTCGCGCGCAG	1200

QY 186 CACCGTTCCGTCGCGAAGTCCCGGCGCTCGGCGTCTTCTGGCGGGATCTGATCCAGAA 245
DB 181 CACCGTTCCGTCGCGAAGTCCCGGCGCTCGGCGTCTTCTGGCGGGATCTGATCCAGAA 240
QY 246 CGGGCCGGTCTGGGGTTGAGTTCCTCGGTGCCAGTGCCTGCGAGCCGACGTCGTCGGC 305
DB 241 CGGGCCGGTCTGGGGTTGAGTTCCTCGGTGCCAGTGCCTGCGAGCCGACGTCGTCGGC 300
QY 306 GCTGTGATCGCGCCCGCTGAGCGTCTCTCGGTCCAAAGTCAAGCACCGTCCCGGGCG 365
DB 301 GCTGTGATCGCGCCCGCTGAGCGTCTCTCGGTCCAAAGTCAAGCACCGTCCCGGGCG 360
QY 366 GATGGATCTATCAGTTCGGCCCTGTGTCGCGAGCCCGCGAGGGCAGCAGTTCGCTCCG 425
DB 361 GATGGATCTATCAGTTCGGCCCTGTGTCGCGAGCCCGCGAGGGCAGCAGTTCGCTCCG 420
QY 426 GCGTCGATCGGGTTGGTCCGTCGCGCCAGCACAGCATCCACCCGAGGTCGAGCAAC 485
DB 421 GCGTCGATCGGGTTGGTCCGTCGCGCCAGCACAGCATCCACCCGAGGTCGAGCAAC 480
QY 486 GGGTCCCGACGGTCACATCTCCAGTTCGATGAACCGCCGAGCTCGGGGACGTCGCGG 545
DB 481 GGGTCCCGACGGTCACATCTCCAGTTCGATGAACCGCCGAGCTCGGGGACGTCGCGG 540
QY 546 CGCAGACGACGTTGTTTCAGATGGCAGTGCCTGTCATGATCCCGGGTTCGGGGTCTGCG 605
DB 541 CGCAGACGACGTTGTTTCAGATGGCAGTGCCTGTCATGATCCCGGGTTCGGGGTCTGCG 600
QY 606 GGGTCGCGAGTCCAGCCAGTCCGCGAGCACATGACACCGAGCAACGACTCGGCGCGG 665
DB 601 GGGTCGCGAGTCCAGCCAGTCCGCGAGCACATGACACCGAGCAACGACTCGGCGCGG 660
QY 666 GGGTCTGATCAGTCTGGGGAGCCGGGTGCCAGCAACCGCGGTGGGAAGCACCCAGAC 725
DB 661 GGGTCTGATCAGTCTGGGGAGCCGGGTGCCAGCAACCGCGGTGGGAAGCACCCAGAC 720
QY 726 CGGGCGATGTCGCGCGAGCAGCCCGAGCCGTCGACCCCGGGAGCCGGGCCCGCGG 785
DB 721 CGGGCGATGTCGCGCGAGCAGCCCGAGCCGTCGACCCCGGGAGCCGGGCCCGCGG 780
QY 786 GACCGGTCTGAGTCCAGCCCGCGCCAGCCCGCGCGGTGCTGATCAGCATCAGCCACCG 845
DB 781 GACCGGTCTGAGTCCAGCCCGCGCCAGCCCGCGCGGTGCTGATCAGCATCAGCCACCG 840
QY 846 GATGGATCTGATCGGCAAGCATCAGCAACAGTAAAGCGTGTTCGGTTGAATCCAATGTG 905
DB 841 GATGGATCTGATCGGCAAGCATCAGCAACAGTAAAGCGTGTTCGGTTGAATCCAATGTG 900
QY 906 CTGTACAGAGGCATCCGATCCGACACACAGCCAGCAGTCCGCAATCTGTCGCG 965
DB 901 CTGTACAGAGGCATCCGATCCGACACACAGCCAGCAGTCCGCAATCTGTCGCG 960
QY 966 ACCCTGGCGTCAAGCGCGTCTGGTCCGCAACCCCGCGCGATGTCGCGCGCGCT 1025
DB 961 ACCCTGGCGTCAAGCGCGTCTGGTCCGCAACCCCGCGCGATGTCGCGCGCGCT 1020
QY 1026 CGGCGCGGCTCTCATGCGCGGTTGTTTCAAGTTCGCTCGTTCGGTGGTGTTCGCGAACG 1085
DB 1021 CGGCGCGGCTCTCATGCGCGGTTGTTTCAAGTTCGCTCGTTCGGTGGTGTTCGCGAACG 1080
QY 1086 GGGCCGCGCGCGTCTGTCGATACGGGATCTATCAGCAGGTAGGCGCTCCAGGC 1145
DB 1081 GGGCCGCGCGCGTCTGTCGATACGGGATCTATCAGCAGGTAGGCGCTCCAGGC 1140
QY 1146 GTACTCTTCGCGCCAGAACAGCGGTGCGTCCGCGCGCAGACAGCGGTCTTCGCGCAG 1205
DB 1141 GTACTCTTCGCGCCAGAACAGCGGTGCGTCCGCGCGCAGACAGCGGTCTTCGCGCAG 1200
QY 1206 ATACACCGAGCGGTGCGCGCATGTCCAGATGTCGCGCAGCGCGCGCGCGCGAG 1265
DB 1201 ATACACCGAGCGGTGCGCGCATGTCCAGATGTCGCGCAGCGCGCGCGCGCGAG 1260

QY 1266 ATCGGATCTATCGCGCGCTGTGCGGGAAGACGAGCGCTAGCGGCGTTGCACTACGTC 1325
DB 1261 ATCGGATCTATCGCGCGCTGTGCGGGAAGACGAGCGCTAGCGGCGTTGCACTACGTC 1320
QY 1326 GCGCGGTTGCGGAGAACGAGCACTATCATCGACCGAGCTTTCGCAACATCGGGCCGTAT 1385
DB 1321 GCGCGGTTGCGGAGAACGAGCACTATCATCGACCGAGCTTTCGCAACATCGGGCCGTAT 1380
QY 1386 CTGCCAGTGTAGGTTCCCGCTCTCGTCCGATCTATCGCGCACCGCGCCCGTCCCGCG 1445
DB 1381 CTGCCAGTGTAGGTTCCCGCTCTCGTCCGATCTATCGCGCACCGCGCCCGTCCCGCG 1440
QY 1446 ACCGCGTGGATCGTTTCGTCAGTACCCGAGGCTCTTTCGAGGCTTAAGCCCAATTGGGAAGAT 1505
DB 1441 ACCGCGTGGATCGTTTCGTCAGTACCCGAGGCTCTTTCGAGGCTTAAGCCCAATTGGGAAGAT 1500
QY 1506 ACTTCGACCTTCCCATCAATAGAGAAAGCATCCCTTAGGGATTCGTCAGCGGGCCG 1565
DB 1501 ACTTCGACCTTCCCATCAATAGAGAAAGCATCCCTTAGGGATTCGTCAGCGGGCCG 1560
QY 1566 GTGTTTCAGTGAACCTTGGCGAGGCAATCCCATCGCGCAGCCCGCGCAGCGAAATC 1625
DB 1561 GTGTTTCAGTGAACCTTGGCGAGGCAATCCCATCGCGCAGCCCGCGCAGCGAAATC 1620
QY 1626 CAC 1628
DB 1621 CAC 1623
RESULT 6
US-10-100-679-88
; Sequence 88, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder;
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c2
; CURRENT APPLICATION NUMBER: US/10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-100-679-88
Query Match 85.4%; Score 1413; DB 14; Length 1413;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ATCTACTCGACCTTCGCCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 65
DB 1 ATCTACTCGACCTTCGCCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 60
QY 66 CTGGCGACCGCTTCGGCGGTTCGCGACGATCAACCGCATGGAAGCAAGCATGTGTGGCC 125
DB 61 CTGGCGACCGCTTCGGCGGTTCGCGACGATCAACCGCATGGAAGCAAGCATGTGTGGCC 120
QY 126 AACGCTGCCCGCATCGCGCAGAGGTGTCGGAACCGGGTCTGCGCGATCTCGCGCCCGG 185
DB 121 AACGCTGCCCGCATCGCGCAGAGGTGTCGGAACCGGGTCTGCGCGATCTCGCGCCCGG 180
QY 186 CACCGTTCGTCGGGGAAGTCCGCGCCTCGCGGTCTTCTGGCGGGATCTGATCCAGAA 245
DB 181 CACCGTTCGTCGGGGAAGTCCGCGCCTCGCGGTCTTCTGGCGGGATCTGATCCAGAA 240

QY 246 CGGCGCGCTCTCGGGTTGAGGTCCTCGGTGCCAGTCCGTCGACGCGACGTCGTCGGC 305
 Db 241 CGGCGCGCTCTCGGGTTGAGGTCCTCGGTGCCAGTCCGTCGACGCGACGTCGTCGGC 300
 QY 306 GCTGGTGATCGCGCGCGTGGGTCCTCGGTCCAAACGTCAGACCGTCGCGCGCGG 365
 Db 301 GCTGGTGATCGCGCGCGTGGGTCCTCGGTCCAAACGTCAGACCGTCGCGCGCGG 360
 QY 366 GATGGATCTATCAGTTCCGCGCTCGGTGCCAGTCCGCGCGCGCGCGACGTCGTCGG 425
 Db 361 GATGGATCTATCAGTTCCGCGCTCGGTGCCAGTCCGCGCGCGCGACGTCGTCGG 420
 QY 426 GCGTCGATCGGTTGGTTCGTCGCGCAGCACACAGCATCCACCGAGTCGAGCAAC 485
 Db 421 GCGTCGATCGGTTGGTTCGTCGCGCAGCACACAGCATCCACCGAGTCGAGCAAC 480
 QY 486 GGGTCCCGGACGGTGCAATCTCCAGTCGATGAACCGCGAGCTCGGGGACGTCGCGG 545
 Db 481 GGGTCCCGGACGGTGCAATCTCCAGTCGATGAACCGCGAGCTCGGGGACGTCGCGG 540
 QY 546 CGCAGCAGCATGTTGTCAGATGCGTCGCGTCGATGATCCCGGGTTCGGGTCGTCG 605
 Db 541 CGCAGCAGCATGTTGTCAGATGCGTCGCGTCGATGATCCCGGGTTCGGGTCGTCG 600
 QY 606 GCGTCGCGAGTCCAGCGAGTCGCGCAGCACATGACCGACGGGACGTCGCGCGG 665
 Db 601 GCGTCGCGAGTCCAGCGAGTCGCGCAGCACATGACCGACGGGACGTCGCGCGG 660
 QY 666 GGATCTCATGCTCGGGGACCGCGGTGCCAGCAACCGCAGCGTGGGAGCACCGAGAC 725
 Db 661 GGATCTCATGCTCGGGGACCGCGGTGCCAGCAACCGCAGCGTGGGAGCACCGAGAC 720
 QY 726 CGGCGCGATGTCGCGCAGCAGCGCCAGCGTCGTCGACCGCGCGGACCGGGCCCGG 785
 Db 721 CGGCGCGATGTCGCGCAGCAGCGCCAGCGTCGTCGACCGCGCGGACCGGGCCCGG 780
 QY 786 GACCGCTCGGAGTCGACCGCGCGCCAGCGCGCGGTGGTGGTACGATCAGCCACCG 845
 Db 781 GACCGCTCGGAGTCGACCGCGCGCCAGCGCGCGGTGGTGGTACGATCAGCCACCG 840
 QY 846 GATGGATCTGATCGGCGAGGATCAGCAACAGTAGCGGTGTCGCGTTGATCCAAATGTG 905
 Db 841 GATGGATCTGATCGGCGAGGATCAGCAACAGTAGCGGTGTCGCGTTGATCCAAATGTG 900
 QY 906 CTGTTCAGCAGCATCCGATGCCGAACACCGACACCGAGCAGTCGCAATCTGTCTCGG 965
 Db 901 CTGTTCAGCAGCATCCGATGCCGAACACCGACACCGAGCAGTCGCAATCTGTCTCGG 960
 QY 966 ACCCTGGGTCACGCGGCGTCTGGTCCGCAACCGCGCGGATGTCGCGCGCGCGCT 1025
 Db 961 ACCCTGGGTCACGCGGCGTCTGGTCCGCAACCGCGCGGATGTCGCGCGCGCGCT 1020
 QY 1026 GCGCGCGCTCTCCATGCGCGGTTGTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1085
 Db 1021 GCGCGCGCTCTCCATGCGCGGTTGTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1080
 QY 1086 GCGCGCGCGCGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1145
 Db 1081 GCGCGCGCGCGCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1140
 QY 1146 GTAATCTTTCGCGCGCGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1205
 Db 1141 GTAATCTTTCGCGCGCGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1200
 QY 1206 ATACACCGCGGTCGCGCGCATGTCAGATCTGGGCGAGCGCGCGCGCATCGGTGGAG 1265
 Db 1201 ATACACCGCGGTCGCGCGCATGTCAGATCTGGGCGAGCGCGCGCGCATCGGTGGAG 1260
 QY 1266 ATCGGATCTATCGCGCGCTGTGGGGAAGGACGAGCGGTAGCGGGTTCGATACGTC 1325
 Db 1261 ATCGGATCTATCGCGCGCTGTGGGGAAGGACGAGCGGTAGCGGGTTCGATACGTC 1320

QY 1326 GCCCGGTTGGCAGAGCAGACTACATCGACCGAGCTTGGCGCAACATCGGCGCGTAT 1385
 Db 1321 GCCCGGTTGGCAGAGCAGACTACATCGACCGAGCTTGGCGCAACATCGGCGCGTAT 1380
 QY 1386 CTGCCAGCTGAGTTCCCGCTCTCGTCGGATCT 1418
 Db 1381 CTGCCAGCTGAGTTCCCGCTCTCGTCGGATCT 1413

RESULT 7
 US-10-607-752-88
 ; Sequence 88, Application US/10607752
 ; Publication No. US20040072224A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Delcayre, Alain
 ; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder
 ; FILE REFERENCE: 11000.1042C3
 ; CURRENT APPLICATION NUMBER: US/10/607,752
 ; CURRENT FILING DATE: 2003-06-26
 ; PRIOR APPLICATION NUMBER: 10/100,679
 ; PRIOR FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 09/450,072
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/351,348
 ; PRIOR FILING DATE: 1999-07-12
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 88
 ; LENGTH: 1413
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium vaccae
 US-10-607-752-88

Query Match 85.4%; Score 1413; DB 18; Length 1413;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1413; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATCTACTCGACCTTCGCGGACCGGGGTACCCGGGTGGCTGACGTACTCGGCGCATCCG 65
 Db 1 ATCTACTCGACCTTCGCGGACCGGGGTACCCGGGTGGCTGACGTACTCGGCGCATCCG 60
 QY 66 CTGGCAGCCGCTCGCGGTTCGCGAGATCAACGCGATGGAAGACGAGCATGTTGGCC 125
 Db 61 CTGGCAGCCGCTCGCGGTTCGCGAGATCAACGCGATGGAAGACGAGCATGTTGGCC 120
 QY 126 AACGTCGCGCATCGCGAGCAGGTCTCGGACCGGTCGCGCATCTCGCGCGCCGG 185
 Db 121 AACGTCGCGCATCGCGAGCAGGTCTCGGACCGGTCGCGCATCTCGCGCGCCGG 180
 QY 186 CACGTTTCGCTCGCGGAGTCCGCGGCTCTTCTGGGCGGATCTGATCCAGAA 245
 Db 181 CACGTTTCGCTCGCGGAGTCCGCGGCTCTTCTGGGCGGATCTGATCCAGAA 240
 QY 246 CGGCGCGCTCTCGCGGTTCGAGTCTCTCGTTCGCGGTCGCGTCGACGCGCATCGTCGGC 305
 Db 241 CGGCGCGCTCTCGCGGTTCGAGTCTCTCGTTCGCGGTCGCGTCGACGCGCATCGTCGGC 300
 QY 306 GCTGGTGATCGCGCGCGGTAGCGTCTCGGTCCCAACGTCAGCACCGTCGCGCGCGG 365
 Db 301 GCTGGTGATCGCGCGCGGTAGCGTCTCGGTCCCAACGTCAGCACCGTCGCGCGCGG 360
 QY 366 GATGGATCTATCAGTTCCGCGCTCGGTGCCAGCGCGCGGCGAGCGCATGTCGCTCCG 425
 Db 361 GATGGATCTATCAGTTCCGCGCTCGGTGCCAGCGCGCGGCGAGCGCATGTCGCTCCG 420
 QY 426 GCGTCGATCGGTTGGTTCGTCGCGCAGCACACAGCATCCACCGAGTCGAGCAAC 485
 Db 421 GCGTCGATCGGTTGGTTCGTCGCGCAGCACACAGCATCCACCGAGTCGAGCAAC 480
 QY 486 GGGTCCCGGACGGTGCAATCTCCAGTCGATGAACCGCGAGCTCGGGGACGTCGCGG 545
 Db 481 GGGTCCCGGACGGTGCAATCTCCAGTCGATGAACCGCGAGCTCGGGGACGTCGCGG 540

```

QY 546 CGCAGCAGCAGCTGTTTCAGATGGCAGTCCCGTGCATGATCCCGGTTCCGGTCTCG 605
Db 541 CGCAGCAGCAGCTGTTTCAGATGGCAGTCCCGTGCATGATCCCGGTTCCGGTCTCG 600
QY 606 GGCCTCGCAGTCCAGCAGTCCGCGAGCAGATGACACGAGCAGGGAACGACTCGGCGCG 665
Db 601 GGCCTCGCAGTCCAGCAGTCCGCGAGCAGATGACACGAGCAGGGAACGACTCGGCGCG 660
QY 666 GGATCTGATCAGTCCGGGAGCGCGGTGCCAGCAACGCGAGCGGTGGGAAGCACCGAGAC 725
Db 661 GGATCTGATCAGTCCGGGAGCGCGGTGCCAGCAACGCGAGCGGTGGGAAGCACCGAGAC 720
QY 726 CGGCGCGATGTCGCGCGCAGCAGCGCCGCGCTGCACCCCGCGGAGCGGCGCCCGCG 785
Db 721 CGGCGCGATGTCGCGCGCAGCAGCGCCGCGCTGCACCCCGCGGAGCGGCGCCCGCG 780
Db 786 GACCGGCTCGGAGTGCACCCCGCGCCAGCAGCGCGCGCGTGGTTCAGCATCAGCCACCG 845
Db 781 GACCGGCTCGGAGTGCACCCCGCGCCAGCAGCGCGCGCGTGGTTCAGCATCAGCCACCG 840
QY 846 GATGGATCTGATCGGCGAGGATCAGCAACAGTAAGCGGTGTTCCGGTTGAATCCAAATGG 905
Db 841 GATGGATCTGATCGGCGAGGATCAGCAACAGTAAGCGGTGTTCCGGTTGAATCCAAATGG 900
QY 906 CTGTGACGAGGATCGATGCCGAAACACCGACACCGGAGCAGTCCGAATCTGTCTCGCG 965
Db 901 CTGTGACGAGGATCGATGCCGAAACACCGACACCGGAGCAGTCCGAATCTGTCTCGCG 960
QY 966 ACCCTGGCGTCAAGCGCGGTGCGGTCCGCAACCCCGCGCGATGTCGCGCGCGCGCT 1025
Db 961 ACCCTGGCGTCAAGCGCGGTGCGGTCCGCAACCCCGCGCGATGTCGCGCGCGCGCT 1020
QY 1026 GCGGCGCGCTCTCCATGGCGGTTCTGATGCTGCTCGTCCGCTGCTGCTGCGAAG 1085
Db 1021 GCGGCGCGCTCTCCATGGCGGTTCTGATGCTGCTCGTCCGCTGCTGCTGCGAAG 1080
QY 1086 GCGGCGCGCGCTGCTGCTGCGATACGGATCTTACCGAGGTAGCGCGTCCAGCC 1145
Db 1081 GCGGCGCGCGCTGCTGCTGCGATACGGATCTTACCGAGGTAGCGCGTCCAGCC 1140
QY 1146 GTACTCTTCCGCCAGAACAGCGGTGCGGTGCGCGCGAGACCGCGTCTGCCGCCAG 1205
Db 1141 GTACTCTTCCGCCAGAACAGCGGTGCGGTGCGCGCGAGACCGCGTCTGCCGCCAG 1200
QY 1206 ATACACCGAGCGGTGCGCGATGTCAGATGTCGTCGCGCGAGCGCGCGCGTGGAG 1265
Db 1201 ATACACCGAGCGGTGCGCGATGTCAGATGTCGTCGCGAGCGCGCGCGTGGAG 1260
QY 1266 ATCGGATCTATCGCGCGGTGTCGGGAGGAGCGGCGGTAGCGCGTTCGACTAGTC 1325
Db 1261 ATCGGATCTATCGCGCGGTGTCGGGAGGAGCGGCGGTAGCGCGTTCGACTAGTC 1320
QY 1326 GCCCGCGTTGGCGAGAGCAGGACTATACGACCGGAGCTTGGCAACATCGGCGCGTAT 1385
Db 1321 GCCCGCGTTGGCGAGAGCAGGACTATACGACCGGAGCTTGGCAACATCGGCGCGTAT 1380
QY 1386 CTGCGAGCTGAGGTTCCCGTCTCTGTCGGATCT 1418
Db 1381 CTGCGAGCTGAGGTTCCCGTCTCTGTCGGATCT 1413

RESULT 8
US-10-100-679-87
; Sequence 87, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c2
; CURRENT APPLICATION NUMBER: US/10/100, 679
; CURRENT FILING DATE: 2002-03-14

```

```

; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
; US-10-100-679-87

Query Match 75.3%; Score 1247; DB 14; Length 1263;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1263; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

QY 6 ATCTACTCGACCTTCGCGACCGGCGGTACCCGGGTGGCTTACGCTACTTCCGGCCATCCG 65
Db 1 ATCTACTCGACCTTCGCGACCGGCGGTACCCGGGTGGCTTACGCTACTTCCGGCCATCCG 60
QY 66 CTGGCGACCGCTCGCGGTGCTCGGACGATCAACGCGATGGAAGACGAAAGGATGTTGGCC 125
Db 61 CTGGCGACCGCTCGCGGTGCTCGGACGATCAACGCGATGGAAGACGAAAGGATGTTGGCC 120
QY 126 AACGCTGCCGATCGGCGAGCAGTGTCTCGGACCGGCTCTCGCGATCTCGCCGCGCG 185
Db 121 AACGCTGCCGATCGGCGAGCAGTGTCTCGGACCGGCTCTCGCGATCTCGCCGCGCG 180
QY 186 CACCGTTGCGTCCGCGAAGTCCGCGCTCGGCGCTTCTCTGGCGGGGATCTGATCCAGAA 245
Db 181 CACCGTTGCGTCCGCGAAGTCCGCGCTCGGCGCTTCTCTGGCGGGGATCTGATCCAGAA 240
QY 246 CGGCGCGGTCTCGCGGTTGAGTCTCGGTGCCAGTCCGTCGACGCGAATCGTCTCGC 305
Db 241 CGGCGCGGTCTCGCGGTTGAGTCTCGGTGCCAGTCCGTCGACGCGAATCGTCTCGC 300
QY 306 GCTGTGATCGCGCGCGTAGGCTCTCTCGGTCCACACGTCAGCAGCGTCCGCGCGCG 365
Db 301 GCTGTGATCGCGCGCGTAGGCTCTCTCGGTCCACACGTCAGCAGCGTCCGCGCGCG 360
QY 366 GATGATCTATCAGTTTCGGCCCTTGGTTCGCGACCGCGCGGAGGCGACGATTCGCTCG 425
Db 361 GATGATC-----TTGCGCCCTTGGTTCGCGACCGCGCGGAGGCGACGATTCGCTCG 414
QY 426 GCGTCGATCGGTTGGTTCGCGTCCGCGCAGCAACAGGATCCACCGGAGTTCGAGCAAC 485
Db 415 GCGTCGATCGGTTGGTTCGCGTCCGCGCAGCAACAGGATCCACCGGAGTTCGAGCAAC 474
QY 486 GGGTCCCGACCGGTGCATCTCCAGTCCGATGAAACCGCGCGAGTCCGCGGAGCTCGCG 545
Db 475 GGGTCCCGACCGGTGCATCTCCAGTCCGATGAAACCGCGCGAGTTCGCGGAGCTCGCG 534
QY 546 CGCAGCAGCAGCTTGTTCAGATGGCAGTCCCGTGCATGATCCCGGTTTCGCGTCTCG 605
Db 535 CGCAGCAGCAGCTTGTTCAGATGGCAGTCCCGTGCATGATCCCGGTTTCGCGTCTCG 594
QY 606 GGCCTCGCGAGTTCAGCGCAGTCCGCGAGCAATGACCGGAGCAACGACTTCGCGCGCG 665
Db 595 GGCCTCGCGAGTTCAGCGCAGTCCGCGAGCAATGACCGGAGCAACGACTTCGCGCGCG 654
QY 666 GGATCTGATCAGTCCGGGAGCGGCGTCCGCGAAGCGCGAGTCCGCGGAGCAGCAGAC 725
Db 655 GGATCTGATCAGTCCGGGAGCGGCGTCCGCGAAGCGCGAGTCCGCGGAGCAGCAGAC 714
QY 726 CGGCGGATGTCGCGCGCAGCAGCGCCGCGTGCACCCCGCGGAGCAGGCGCCCGCG 785
Db 715 CGGCGGATGTCGCGCGCAGCAGCGCCGCGTGCACCCCGCGGAGCAGGCGCCCGCG 774
QY 786 GACCGCGTCCGAGTTCAGACCCCGCGCGCAACCGCGCGCGTGGTTCAGCATCAGCCACCG 845
Db 775 GACCGCGTCCGAGTTCAGACCCCGCGCGCAACCGCGCGCGTGGTTCAGCATCAGCCACCG 834

```



```
QY 1266 ATCGGATCT 1274
Db 1255 ATCGGATCT 1263

RESULT 10
US-10-100-679-86
; Sequence 86, Application US/10100679
; Publication No. US2003054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c2
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-10-100-679-86

Query Match 67.4%; Score 1116; DB 14; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.7e-288;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATCTACTCGACCTTCGCCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 65
Db 1 ATCTACTCGACCTTCGCCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 60

QY 66 CTGGGACCGCTTCGCGGTTCGCGATCAACCGCATGGAAGCAAGGATGTGGCC 125
Db 61 CTGGGACCGCTTCGCGGTTCGCGATCAACCGCATGGAAGCAAGGATGTGGCC 120

QY 126 AACGCTGCCCGATCGCGGAGCAGGTCTCGGACCGGGTCTGCGCATCTCGCGCCCGG 185
Db 121 AACGCTGCCCGATCGCGGAGCAGGTCTCGGACCGGGTCTGCGCATCTCGCGCCCGG 180

QY 186 CACCGTTCCGTCGGCGAAGTCCCGGCTCGCGTCTTCTGGCGGGATCTGATCCAGAA 245
Db 181 CACCGTTCCGTCGGCGAAGTCCCGGCTCGCGTCTTCTGGCGGGATCTGATCCAGAA 240

QY 246 CGGGCCGGTCTCGGGTTGAGGTCTCGGTGCGCATGCCGTGCGACGACGTGTCGGC 305
Db 241 CGGGCCGGTCTCGGGTTGAGGTCTCGGTGCGCATGCCGTGCGACGACGTGTCGGC 300

QY 306 GCTGTGTGATCGGCGCGCGGTAGCGTCTCGGTCCACAGTCACAGTCGACCGTCCGCGGCG 365
Db 301 GCTGTGTGATCGGCGCGCGGTAGCGTCTCGGTCCACAGTCACAGTCGACCGTCCGCGGCG 360

QY 366 GATGGATCTATCAGTTTCGGCCCTTGGTTCGGCAGCGCCCGGAGGCGACGATTCGCTCCG 425
Db 361 GATGGATCTATCAGTTTCGGCCCTTGGTTCGGCAGCGCCCGGAGGCGACGATTCGCTCCG 420

QY 426 GCSTCATCGGTTGGTTCGTCGGCGCAGCAACACAGATCCACCGAGGTGCGAGCAAC 485
Db 421 GCSTCATCGGTTGGTTCGTCGGCGCAGCAACACAGATCCACCGAGGTGCGAGCAAC 480

QY 486 GGGTCCCGACGGTGCACATCTCCAGTGCATGAACCGCGCAGCTCGGGAGCTCGCG 545
Db 481 GGGTCCCGACGGTGCACATCTCCAGTGCATGAACCGCGCAGCTCGGGAGCTCGCG 540

QY 546 CGCAGCAGCAGTGTGTTTCAGATGGCAGTGCCTGATGATCCCGGTTTCGGCGTCTCG 605
Db 546 CTGGGACCGCTTCGGCGGTTCGCGATCAACGCGATCAACGCGATGGAAGCAAGGATGTGGCC 125
```

```
Db 61 CTGGGACCCCTCGCGCTCGGAGATCAACGCGATGGAAGCAATGCTGGCC 120
Qy 126 AAGCTGCCGATCGCGAGAGAGTCTCGGACCGGCTCTGCGCATCTCGCGCGCCG 185
Db 121 AAGCTGCCGATCGCGAGAGAGTCTCGGACCGGCTCTGCGCATCTCGCGCGCCG 180
Qy 186 CACGTTCCGTCGGCGAAGTCCGCGCTCGGCTCTTCTGGGCGGATCTGATCAGAA 245
Db 181 CACGTTCCGTCGGCGAAGTCCGCGCTCGGCTCTTCTGGGCGGATCTGATCAGAA 240
Qy 246 CGGCGCGCTCTCGGGTTGAGGTCCTCGGTGCCAGTCCGTCGACGCGAGTCTGCGC 305
Db 241 CGGCGCGCTCTCGGGTTGAGGTCCTCGGTGCCAGTCCGTCGACGCGAGTCTGCGC 300
Qy 306 GCTGGTATCGCGCGCGCTGAGGCTCTCGGTCCACAACTCAGCACCGTCCCGGGG 365
Db 301 GCTGGTATCGCGCGCGCTGAGGCTCTCGGTCCACAACTCAGCACCGTCCCGGGG 360
Qy 366 GATGGATCTATCAGTTCGGCCCTGTCGCGAGCCCGGAGGGCAGCAGTTCGGCTCC 425
Db 361 GATGGATCTATCAGTTCGGCCCTGTCGCGAGCCCGGAGGGCAGCAGTTCGGCTCC 420
Qy 426 GCGTCGATCGGTTGGTTCGTCGCGCAGCACACACAGCATCCACCGAGTTCGAGCAAC 485
Db 421 GCGTCGATCGGTTGGTTCGTCGCGCAGCACACACAGCATCCACCGAGTTCGAGCAAC 480
Qy 486 GGGTCCCGACGCTGACATCTCCAGTCGATGAAACCGCGAGCTCGGGAGAGTTCGCG 545
Db 481 GGGTCCCGACGCTGACATCTCCAGTCGATGAAACCGCGAGCTCGGGAGAGTTCGCG 540
Qy 546 GCGAGCAGCAGTGTTCAGATGCGAGTCGCGTGCATGATCCCGGTTCTGGGTCGTCG 605
Db 541 GCGAGCAGCAGTGTTCAGATGCGAGTCGCGTGCATGATCCCGGTTCTGGGTCGTCG 600
Qy 606 GGCCTGCGCAGTTCAGCAGTTCGCGCAGCACATGACCGAGCGGAAACGATTCGGCGCG 665
Db 601 GGCCTGCGCAGTTCAGCAGTTCGCGCAGCACATGACCGAGCGGAAACGATTCGGCGCG 660
Qy 666 GGATCTGATCAGTCTCGGGAGCGGGTGCAGCAAGCCAGCGTGGGAGACCGAGAC 725
Db 661 GGATCTGATCAGTCTCGGGAGCGGGTGCAGCAAGCCAGCGTGGGAGACCGAGAC 720
Qy 726 CGGCGCATGTGCCCGCAGCAGCGCCAGCGCTGACCCCGCGGACCGGGCCCGCG 785
Db 721 CGGCGCATGTGCCCGCAGCAGCGCCAGCGCTGACCCCGCGGACCGGGCCCGCG 780
Qy 786 GACCGCTCGAGTTCGACCCCGCGCCAGCCCGCGCGCTGTCAGCATCAGCCACCG 845
Db 781 GACCGCTCGAGTTCGACCCCGCGCCAGCCCGCGCGCTGTCAGCATCAGCCACCG 840
Qy 846 GATGGATCTGATCGGAGGATACGAAACAGTAAGCGGTTCGCGTTGAATCCAAATGTG 905
Db 841 GATGGATCTGATCGGAGGATACGAAACAGTAAGCGGTTCGCGTTGAATCCAAATGTG 900
Qy 906 CTGTACGAGCATCCGATCCGAAACACCGACCGAGCAGTCCGAACTGTCTCGCG 965
Db 901 CTGTACGAGCATCCGATCCGAAACACCGACCGAGCAGTCCGAACTGTCTCGCG 960
Qy 966 ACCCTGGGTCACGCGCGCTGTCGCTCCGAAACCGCGCGGATGTCGCGCGCGCGCT 1025
Db 961 ACCCTGGGTCACGCGCGCTGTCGCTCCGAAACCGCGCGGATGTCGCGCGCGCGCT 1020
Qy 1026 CGGCGCGCTCTCCATGCGCGTTCTGTTAGTCGCTGTCGCGTGGCTGTTCTCGAAACG 1085
Db 1021 CGGCGCGCTCTCCATGCGCGTTCTGTTAGTCGCTGTCGCGTGGCTGTTCTCGAAACG 1080
Qy 1086 GCGCGCGCGCTCTCGCTCCGATACGGGATCT 1121
Db 1081 GCGCGCGCGCTCTCGCTCCGATACGGGATCT 1116
```

RESULT 12

```
US-10-100-679-56
; Sequence 56, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder
; FILE REFERENCE: 11000.1042G2
; CURRENT APPLICATION NUMBER: US/10/100,679
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-100-679-56
```

```
Query Match 61.1%; Score 1011.4; DB 14; Length 1749;
Best Local Similarity 78.9%; Pred. No. 1.6e-260;
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;

Qy 1 GATCTATCTACTCGACCTTCGCGACCGGGCTGACCGGGTGGCTTACGCTACTCCGGCC 60
Db 95 GATCTATCTACTCGACCTTCGCGACCGGGCTGACCGGGTGGCTTACGCTACTCCGGCC 154
Qy 61 ATCCGCTGGCGACCGCTTCGCGAGCATCAACGCGATGGAAGAGGATGG 120
Db 155 ATCCGCTGGCGACCGCTTCGCGAGCATCAACGCGATGGAAGAGGATGG 214
Qy 121 TGCCCAACGCTCCCGCATCGCGAGCAGGTGCTCGGACCGGGTCTCGCGATCTCGCG 180
Db 215 TGCCCAACGCTCCCGCATCGCGAGCAGGTGCTCGGACCGGGTCTCGCGATCTCGCG 274
Qy 181 CCGGCAACGCTTCGCTCGCGAAGTCCGCGCTTCGCGCTTCTTCTGGCGGGATCTGATC 240
Db 275 CCGGCAACGCTTCGCTCGCGAAGTCCGCGCTTCTTCTGGCGGGATCTGATC 334
Qy 241 CAGAACGGGCGGCTTCGCGGTTGAGTCTCTCGGTGCCAGTGCCTCGACGCGACGTCG 300
Db 335 CAGAACGGGCGGCTTCGCGGTTGAGTCTCTCGGTGCCAGTGCCTCGACGCGACGTCG 394
Qy 301 TCGGCGCTGTGATTCGGCGCGCTAGGCTGCTTCGCTCCACACGTCAGCACCGTGCCC 360
Db 395 TCGGCGCTGTGATTCGGCGCGCTAGGCTGCTTCGCTCCACACGTCAGCACCGTGCCC 454
Qy 361 GGGCGGATGATCTTATCAGTTCGGCTTCGTCAGCCCGCGAGGCGAGCCAGTTCCG 420
Db 455 GGGCGGATGATCTTATCAGTTCGGCTTCGTCAGCCCGCGAGGCGAGCCAGTTCCG 510
Qy 421 CTCGGCGCTCGATCGGGTTGGTCCGTCGGCGCAGCACACGAGATCCACCGGAGTTCGA 480
Db 511 TCCAAATGTGTGTGAGCAGGATCCGA-----TGCGGAAACACGACCGCGAGATC 564
Qy 481 GCAACGGTCCCGACGGTGCATCTCCAGTCGATGAAACGCGCGAGCTCGGGAGCT 540
Db 565 GCAATCTGTCTTCGCGACCCCTGGCGTTCAGCGGCGCTGCTGCTCCGAAACCGCGCGGAT 624
Qy 541 CGCGCGCAGCAGCAGCTTGTTCAGATGGAGTTCGCGTGCATGATCCCGGTTTCGGCGT 600
Db 625 GTCGCGCGCGCGT-----GCGCGCGCTCTCCATGGCGGTTTCGTTTCACT 671
Qy 601 CGTCGGGCTTCGCGAGTTCAGCGCAGTTCGCGGAGCAGATGACCGAGCGGAAACGACTCGG 660
Db 672 CGTCGTCGCTGCTGTTCTGCGAAACGGGCGCGCGCGCTGCTCG-----TCCG 724
```

661 GCACGGGATCTGATAGCTCGGGAGCGGGTCCCGACGAAACCGCAGCGTGGGAACACC 720
Db |||||
725 ATACGGGATCTGATAGCTCGGGAGCGGGTCCCGACGAAACCGCAGCGTGGGAACACC 784
Qy |||||
721 GAGACGGGGGATGTGCGCGCAGCAGCGCCAGCGTGCACCCCGCGGAGACCGGGCC 780
Db |||||
785 GAGACGGGGGATGTGCGCGCAGCAGCGCCAGCGTGCACCCCGCGGAGACCGGGCC 844
Qy |||||
781 CCGCGAGCCGCTCGGAGTGCACCCCGCGCGCACCGCGCGCGTGTGTGAGCATCAGC 840
Db |||||
845 CCGCGAGCCGCTCGGAGTGCACCCCGCGCGCACCGCGCGCGTGTGTGAGCATCAGC 904
Qy |||||
841 CACGGATGATCT 896
Db |||||
905 CACGGATGATCTATCAGTGTGGCCCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 964
Qy |||||
897 TCCAAATGTGTGTCAGCAGGCATCCGA-----TGCAGAACCCGACCGAGCAGTC 950
Db |||||
965 CTCGGGCTCGATCGGGTGGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1024
Qy |||||
951 GCAATCTGTCTCGGACCTTGGGCTCAGCGGGTCTGTGTCTCTCTCTCTCTCTCTCTCT 1010
Db |||||
1025 GCAACGGGTCCTCGGAGTGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1084
Qy |||||
1011 GTCGGGGCGCCGCT-----GGGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1057
Db |||||
1085 CGCGGGCGCAGCAGCATGTTTTCAGATGGCAGTCTCGCGCTGCAATGATCCCGGGTTCGGCGCT 1144
Qy |||||
1058 CGCTCTGTCTCGGTCGGCTTCTCTGGAAGGGGCGCGCGCGCGCGCTCTCTCTCTCTCT 1110
Db |||||
1145 CGTCGGGCTCTCGGAGTTCAGCCAGTTCGGCGAGCATGACCCAGCGGAGCATCTCGG 1204
Qy |||||
1111 ATACGGGATCTATCAGCAGGTAGCGGCTCCAGCGCTACTCTCTCTCTCTCTCTCTCTCT 1170
Db |||||
1205 CGCGGGATCTATCAGCAGGTAGCGGCTCCAGCGCTACTCTCTCTCTCTCTCTCTCTCT 1264
Qy |||||
1171 GCGGTCTCGCGCAGACACCGGTCTCTCGGACAGATACACCCAGCGGTGGCGGCATG 1230
Db |||||
1265 GCGGTCTCGCGCAGACACCGGTCTCTCGGACAGATACACCCAGCGGTGGCGGCATG 1324
Qy |||||
1231 TCAGATCTGTGGCAGCGCGCGCAGCGTGGAGATCGGATCTATCTCGCGCGCTCTGCG 1290
Db |||||
1325 TCAGATCTGTGGCAGCGCGCGCAGCGTGGAGATCGGATCTATCTCGCGCGCTCTGCG 1384
Qy |||||
1291 GGAAGGACGAGCGCTAGCGCGCTTGCACTACGTCTCGCGCGCTTGCGAGACGAGACT 1350
Db |||||
1385 GGAAGGACGAGCGCTAGCGCGCTTGCACTACGTCTCGCGCGCTTGCGAGACGAGACT 1444
Qy |||||
1351 ACATCGACCGAGCTTGGCGAAATCGGGCGGTATCTGCCAGCTGAGGTTCCCGCTCTCG 1410
Db |||||
1445 ACATCGACCGAGCTTGGCGAAATCGGGCGGTATCTGCCAGCTGAGGTTCCCGCTCTCG 1504
Qy |||||
1411 TCAGATCTATCGCGCCACCGCGCGGTGCGCGCAGCGGTGGATCTGTTCTGTCAGTACC 1470
Db |||||
1505 TCAGATCTATCGCGCCACCGCGCGGTGCGCGCAGCGGTGGATCTGTTCTGTCAGTACC 1564
Qy |||||
1471 CGAAGCTCTTTGAGAGCTAAGGCCAAATGGGAAGATCTTGGACCTTCCCATCAATAGAGG 1530
Db |||||
1565 CGAAGCTCTTTGAGAGCTAAGGCCAAATGGGAAGATCTTGGACCTTCCCATCAATAGAGG 1624
Qy |||||
1531 AAAAGCATCGCCCTAGGGATCTGTAGCGGGCGCGGTGTTTCAGTGAACCTTGGCGAGG 1590
Db |||||
1625 AAAAGCATCGCCCTAGGGATCTGTAGCGGGCGCGGTGTTTCAGTGAACCTTGGCGAGG 1684
Qy |||||
1591 CAATCCCATCGCGGACCGCGCAGCGGAATTCACAGGATCCCATCAATCAATCACCATC 1650
Db |||||
1685 CAATCCCATCGCGGACCGCGCAGCGGAATTCACAGGATCCCATCAATCAATCACCATC 1744
Qy |||||
1651 ACTGA 1655
Db |||||
1745 ACTGA 1749

RESULT 13
US-10-607-752-56
; Sequence 56, Application US/10607752
; Publication No. US2004007224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder:
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; TYPE: DNA
; LENGTH: 1749
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-607-752-56

Query Match 61.1%; Score 1011.4; DB 18; Length 1749;
Best Local Similarity 78.9%; Pred. No. 1.6e-260;
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;

Qy 1 GATCTATCTACTCGACCTTCGCGACCGGGTACCGGGTGGCTTACGATCTCCGGCC 60
Db 95 GATCTATCTACTCGACCTTCGCGACCGGGTACCGGGTGGCTTACGATCTCCGGCC 154
Qy 61 ATCCGCTGCGACCGGCTGCGCGGTGCGACCATCAACCGATGGAAGACGAAGGATGG 120
Db 155 ATCCGCTGCGACCGGCTGCGCGGTGCGACCATCAACCGATGGAAGACGAAGGATGG 214
Qy 121 TGGCCAAACGCTCCGCGATCGCGAGCAGGTGCTCGAACCGGGTCTGCGGATCTCGCG 180
Db 215 TGGCCAAACGCTCCGCGATCGCGAGCAGGTGCTCGAACCGGGTCTGCGGATCTCGCG 274
Qy 181 CCGGACACGCTTCGCTGCGGAGTCCGCGGCTCGCGCTCTCTCGGGGGGATCTGATC 240
Db 275 CCGGACACGCTTCGCTGCGGAGTCCGCGGCTCGCGCTCTCTCGGGGGGATCTGATC 334
Qy 241 CAGAACGGCGCGCTCTCGGGTTGAGGTCTCTCGGTCCCGAGTCCCGTCGACGCGAGTCG 300
Db 335 CAGAACGGCGCGCTCTCGGGTTGAGGTCTCTCGGTCCCGAGTCCCGTCGACGCGAGTCG 394
Qy 301 TCGCGCTCTGTATGCGCGCGCGGTAGGCTCTCGGTCCAAACGTCAGACCGGTGCC 360
Db 395 TCGCGCTCTGTATGCGCGCGCGGTAGGCTCTCGGTCCAAACGTCAGACCGGTGCC 454
Qy 361 GGGCGATGATCTATCAGTTCGGCTTGGCTCGCGAGCCCGCGAGGCGAGCTTCG 420
Db 455 GGGCGATGATCT 510
Qy 421 CTCGGCGCTCGATCGGGTTGGGTCTCGCGCGCAGCACACCGAGCATCTCCCGAGTCTGA 480
Db 511 TCCAAATGCTGTACAGGATCTCGA-----TGCAGAACCCGACCGAGCAGTC 564
Qy 481 GCAACGGGTCCCGACCGGTGCAATCTCCAGTTCAGTAAACCGCGGAGCTCGGGGACGT 540
Db 565 GCAATCTGTCTCGGACCGCTGCGGTCAACCGGGTCTGCGTCCGAAACCGCGCGCAT 624
Qy 541 CCGGGCGCAGCAGCATGTTGTTTCAGATGCGCGCTGCTGATGATCCCGGGTTCGGCGT 600
Db 625 GTCGCGCGCGCT-----GGGGCGGCTCTCTCATGGCGGTTCTGTTGAT 671
Qy 601 CGTCGGGCTTCGCGAGTCCAGCTCGCGCAGCAGCATGTCACCGAGCGGAACTCGG 660

Db 601 GGGCTGGCGAGTCCAGCCAGTCCGGAGCACAATGACCGAGCGGAACGACTCCGGGCGG 660
QY 666 GGATCTGATCAGCTCGGGGAGCGGGTGCCAGCAACCGCAGCGTGGGAAGCACCCGAGAC 725
Db 661 GGATCTGATCAGCTCGGGGAGCGGGTGCCAGCAACCGCAGCGTGGGAAGCACCCGAGAC 720
QY 726 CGGCGGATGTGCCCGGAGCAGCGCCAGCCGCTGCACCCCGGAGCCGGGCCCGCG 785
Db 721 CGGCGGATGTGCCCGGAGCAGCGCCAGCCGCTGCACCCCGGAGCCGGGCCCGCG 780
QY 786 GACCGGCTCGGAGTGCACCCCGCCAGCCCGCGCGCTGCTCAGCATCAGCCACCG 845
Db 781 GACCGGCTCGGAGTGCACCCCGCCAGCCCGCGCGCTGCTCAGCATCAGCCACCG 840
QY 846 GAT 848
841 GAT 843

RESULT 15
US-10-607-752-85
; Sequence 85, Application US/10607752
; Publication No. US20040072224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; TYPE: DNA
; LENGTH: 843
; ORGANISM: Mycobacterium vaccae
US-10-607-752-85

Query Match 50.9%; Score 843; DB 18; Length 843;
Best Local Similarity 100.0%; Pred. No. 1.7e-215;
Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 6 ATCTACTCGACCTTCGCCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 65
Db 1 ATCTACTCGACCTTCGCCGACCGGGGTACCCGGGTGGCTGACGTACTCCGGCCATCCG 60
QY 66 CTGGCAGCCGCTCGCGGTTCGGGATCAACCGCATGGAAGACGAAGGCATGTGGCC 125
Db 61 CTGGCAGCCGCTCGCGGTTCGGGATCAACCGCATGGAAGACGAAGGCATGTGGCC 120
QY 126 AAGCTGCCCGCATCGCGAGCAGGTCTCGGACCGGGTCTGCGGATCTCGCGCCCGCG 185
Db 121 AAGCTGCCCGCATCGCGAGCAGGTCTCGGACCGGGTCTGCGGATCTCGCGCCCGCG 180
QY 186 CACGTTTCGGTTCGGCGAAGTCCGCGGCTTCGCGGCTCTTCGGCGGGATCTGATCCAGAA 245
Db 181 CACGTTTCGGTTCGGCGAAGTCCGCGGCTTCGCGGCTCTTCGGCGGGATCTGATCCAGAA 240
QY 246 CGGCGCGGTCTGCGGGTTGAGGTCTCTCGGTGCCAGTGCCTCGACCGCAGCTCGTCGGC 305
Db 241 CGGCGCGGTCTGCGGGTTGAGGTCTCTCGGTGCCAGTGCCTCGACCGCAGCTCGTCGGC 300
QY 306 GCTGGTGTATGCGGCGCGGTAGGGTCTCTCGGTGCCAGTGCCTCGACCGCAGCTCGTCGGCGG 365
Db 301 GCTGGTGTATGCGGCGCGGTAGGGTCTCTCGGTGCCAGTGCCTCGACCGCAGCTCGTCGGCGG 360

QY 366 GATGATCTATCAGTTCCGGCCTCGTCCAGCCCGCCGAGGGCAGCCAGTTCCGCTCCG 425
Db 361 GATGATCTATCAGTTCCGGCCTCGTCCAGCCCGCCGAGGGCAGCCAGTTCCGCTCCG 420
QY 426 GCGTCGATCGGGTTGGTCCGTCGCGCCAGCAACACAGCATCCACCCGAGGTTCGAGCAAC 485
Db 421 GCGTCGATCGGGTTGGTCCGTCGCGCCAGCAACACAGCATCCACCCGAGGTTCGAGCAAC 480
QY 486 GGGTCCCGACCGTTCACATCTCCAGTGCATGAAACCGCGCGAGCTCCGGGACGTCGCGG 545
Db 481 GGGTCCCGACCGTTCACATCTCCAGTGCATGAAACCGCGCGAGCTTCGGGACGTCGCGG 540
QY 546 CGCAGCAGCACGTTGTTTTCAGATGCGCGTGCATGATCCCGGGTTTCGGGCTCGTCG 605
Db 541 CGCAGCAGCACGTTGTTTTCAGATGCGCGTGCATGATCCCGGGTTTCGGGCTCGTCG 600
QY 606 GGCCTGCGCAGTCCAGCCAGTCCGGGAGCAATGACCGGAGGAAACGACTTCGGGCGCG 665
Db 601 GGCCTGCGCAGTCCAGCCAGTCCGGGAGCAATGACCGGAGGAAACGACTTCGGGCGCG 660
QY 666 GGATCTGATCAGTCCGGGAGCGGGTGCCAGCAACCGCAGCGTGGGAAGCACCGAGAC 725
Db 661 GGATCTGATCAGTCCGGGAGCGGGTGCCAGCAACCGCAGCGTGGGAAGCACCGAGAC 720
QY 726 CGGCGCATGTGCCCGCGCAGCAGCGCCAGCCGCTGTCACCCCGCGGACCCGGGCCCGCGG 785
Db 721 CGGCGCATGTGCCCGCGCAGCAGCGCCAGCCGCTGTCACCCCGCGGACCCGGGCCCGCGG 780
QY 786 GACCGGCTCGGAGTGCACCCCGCGCGCACCAGCGCGCGCTGCTCAGCATCAGCCACCG 845
Db 781 GACCGGCTCGGAGTGCACCCCGCGCGCACCAGCGCGCGCTGCTCAGCATCAGCCACCG 840
QY 846 GAT 848
841 GAT 843

Search completed: October 7, 2005, 00:25:23
Job time : 1120 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 20:31:57 ; Search time 310 Seconds
(without alignments)
8735.606 Million cell updates/sec

Title: US-10-607-752-115

Perfect score: 1655

Sequence: 1 gatctatctactgaccttc.....atccaccatcaccatcactga 1655

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1655	100.0	1749	3	US-09-450-072-58
2	1655	100.0	1749	3	US-09-351-348-58
3	1011.4	61.1	1749	3	US-09-450-072-56
4	1011.4	61.1	1749	3	US-09-351-348-56
5	740.2	44.7	1749	3	US-09-450-072-57
6	740.2	44.7	1749	3	US-09-351-348-57
7	291	17.6	291	3	US-09-450-072-15
8	291	17.6	291	3	US-09-351-348-15
9	261	15.8	261	3	US-09-450-072-18
10	261	15.8	261	3	US-09-351-348-18
11	226	13.7	697	3	US-09-450-072-14
12	226	13.7	697	3	US-09-351-348-14
13	210	12.7	210	3	US-09-450-072-13
14	210	12.7	210	3	US-09-351-348-13
15	177	10.7	177	3	US-09-450-072-21
16	177	10.7	177	3	US-09-351-348-21
17	147	8.9	147	3	US-09-450-072-16
18	147	8.9	147	3	US-09-351-348-16
19	138	8.3	138	3	US-09-450-072-17
20	138	8.3	138	3	US-09-351-348-17
21	132	8.0	132	3	US-09-450-072-20
22	132	8.0	132	3	US-09-351-348-20
23	114	6.9	114	3	US-09-450-072-11
24	114	6.9	114	3	US-09-351-348-11
25	96	5.8	96	3	US-09-450-072-9
26	96	5.8	96	3	US-09-351-348-9
27	95.6	5.8	1245	4	US-09-489-039A-6149

c

ALIGNMENTS

RESULT 1

US-09-450-072-58

; Sequence 58, Application US/09450072

; Patent No. 6358734

; GENERAL INFORMATION:

; APPLICANT: Delcayre, Alain

; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder

; FILE REFERENCE: 11000.1042c1

; CURRENT APPLICATION NUMBER: US/09/450,072

; CURRENT FILING DATE: 1999-11-29

; EARLIER APPLICATION NUMBER: 09/351,348

; EARLIER FILING DATE: 1999-07-12

; NUMBER OF SEQ ID NOS: 81

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 58

; LENGTH: 1749

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Made in a lab

US-09-450-072-58

Query Match	100.0%;	Score 1655;	DB 3;	Length 1749;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1655;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GATCTATCTACTCGACCTTCGCGACCGCGCGGTACCGCGGTGGCGCTGACGCTACTTCCGGCC	60	
Db	95	GATCTATCTACTCGACCTTCGCGACCGCGCGGTACCGCGGTGGCGCTGACGCTACTTCCGGCC	154	
Qy	61	ATCCGCTGGCGACCGCGCTTCGCGACGATCAACGCGATGGAAGACGAGCATGG	120	
Db	155	ATCCGCTGGCGACCGCGCTTCGCGACGATCAACGCGATGGAAGACGAGCATGG	214	
Qy	121	TGGCCAAACGCTGCCCGCATCGCGAGCAGGTCTCGGACCGCGGTCTGGCGGATCTCCCG	180	
Db	215	TGGCCAAACGCTGCCCGCATCGCGAGCAGGTCTCGGACCGCGGTCTGGCGGATCTCCCG	274	
Qy	181	CCGCGACCGCTTCGGTTCGGCGGAGTCCGCGCGCTTCCTCTGGCGGGATCTGATC	240	
Db	275	CCGCGACCGCTTCGGTTCGGCGGAGTCCGCGCGCTTCCTCTGGCGGGATCTGATC	334	
Qy	241	CAGAACCGCGCGGTCTCGCGGTTGAGGTCTTCGCTGCCAGTCCGCTCGACGCGACGTCG	300	
Db	335	CAGAACCGCGCGGTCTCGCGGTTGAGGTCTTCGCTGCCAGTCCGCTCGACGCGACGTCG	394	
Qy	301	TCGCGCGTGTGATGCGCGCGCGCGTCTCGGTCCCAACAGTCAGCACCGTCCGC	360	
Db	395	TCGCGCGTGTGATGCGCGCGCGCGTCTCGGTCCCAACAGTCAGCACCGTCCGC	454	

QY 361 GGGGGATGATCTATCAGTTCCGGCCCTGGTCCGACGCGCGGAGGAGCAGCTTCGG 420
 Db 455 GGGCGATGATCTATCAGTTCCGGCCCTGGTCCGACGCGCGGAGGAGCAGCTTCGG 514
 QY 421 CTCGGCGTCCGATCGGGTGGGTCCTGCGCGGCGAGCAGCAGCAGCTCCACCCGAGGTCCA 480
 Db 515 CTCGGCGTCCGATCGGGTGGGTCCTGCGCGGCGAGCAGCAGCAGCTCCACCCGAGGTCCA 574
 QY 481 GCAACGGGTCCCGACGGGTGCAATCTCCAGTTCGATGAACGCGGAGCTCCGGGACGCT 540
 Db 575 GCAACGGGTCCCGACGGGTGCAATCTCCAGTTCGATGAACGCGGAGCTCCGGGACGCT 634
 QY 541 CGCGGCGCAGCAGCAGCTGGTTTCAGATGGGAGTCCGCGTGCATGATCCCGGTTCCGGCT 600
 Db 635 CGCGGCGCAGCAGCAGCTGGTTTCAGATGGGAGTCCGCGTGCATGATCCCGGTTCCGGCT 694
 Db 601 CGTCGGGCTTCGCGAGTCCAGCAGTCGCGGAGCAGCAGTCCAGCAGGAGCAGCTCCG 660
 Db 695 CGTCGGGCTTCGCGAGTCCAGCAGTCGCGGAGCAGCAGTCCAGCAGGAGCAGCTCCG 754
 QY 661 GCGCGGATCTGATCAGCTCGGGAGCGGGTCCAGCAACGCCAGCGTGGGAAGCACC 720
 Db 755 GCGCGGATCTGATCAGCTCGGGAGCGGGTCCAGCAACGCCAGCGTGGGAAGCACC 814
 QY 721 GAGACGGGCGGATGTCGCGCGCAGCAGCGCCGCGGCGTGCACCCCGGGGACCGGGC 780
 Db 815 GAGACGGGCGGATGTCGCGCGCAGCAGCGCCGCGGCGTGCACCCCGGGGACCGGGC 874
 QY 781 CCGCGGACCGCTCGGAGTCCAGCAGTCCGCGCGCAGCAGCGCGCGTGCAGCATCAGC 840
 Db 875 CCGCGGACCGCTCGGAGTCCAGCAGTCCGCGCGCAGCAGCGCGCGTGCAGCATCAGC 934
 QY 841 CACGGGATGATCTGATCGGAGGATCAGCAACAGTAAAGCGGTTCGCGTTGAATCCA 900
 Db 935 CACGGGATGATCTGATCGGAGGATCAGCAACAGTAAAGCGGTTCGCGTTGAATCCA 994
 QY 901 ATGCTGTTCAGCAGCAGTCCGATGCGACACCGACCGCAGCAGTCCGCAATCTGTC 960
 Db 995 ATGCTGTTCAGCAGCAGTCCGATGCGACACCGACCGCAGCAGTCCGCAATCTGTC 1054
 QY 961 TCAGGACCTTCGCGGCTCAGCGGCGTTCGCTCCGCAACCGCGCGGCGATGTCGCGCGG 1020
 Db 1055 TCAGGACCTTCGCGGCTCAGCGGCGTTCGCTCCGCAACCGCGCGGATGTCGCGCGG 1114
 QY 1021 CCGCTCGGCGGCTTCGATGCGCGGTTTCGTTTCAGTCCGTCGCTCCGTTGCTTCGTC 1080
 Db 1115 CCGCTCGGCGGCTTCGATGCGCGGTTTCGTTTCAGTCCGTCGCTCCGTTGCTTCGTC 1174
 QY 1081 GAACGGGCGCGCGCGCTTCGTCGATACGGGATCTATCAGCAGGTAGGCGCTC 1140
 Db 1175 GAACGGGCGCGCGCGCTTCGTCGATACGGGATCTATCAGCAGGTAGGCGCTC 1234
 QY 1141 CAGCGCTACTCTTCGCGCCAGAACAGCGGTTCGCTCCGCGCAGACAGCGTCTCTGCC 1200
 Db 1235 CAGCGCTACTCTTCGCGCCAGAACAGCGGTTCGCTCCGCGCAGACAGCGTCTCTGCC 1294
 QY 1201 GCAGATACACCGAGCGGTGGCGGATGTCAGATGCTGCGCGCAGCGCGCGGACAGG 1260
 Db 1295 GCAGATACACCGAGCGGTGGCGGATGTCAGATGCTGCGCGCAGCGCGCGGACAGG 1354
 QY 1261 TGGAGATCGGATCTATTCGCGCGCTGTCGCGGAGGACGAGGCGGTAGCGGCTTCGACT 1320
 Db 1355 TGGAGATCGGATCTATTCGCGCGCTGTCGCGGAGGACGAGGCGGTAGCGGCTTCGACT 1414
 QY 1321 ACCTCGCGCGGTTCGCGAGAACAGGACTATCAGCAGCGGCTTCGCGCAACATCGGGC 1380
 Db 1415 ACCTCGCGCGGTTCGCGAGAACAGGACTATCAGCAGCGGCTTCGCGCAACATCGGGC 1474
 QY 1381 CGTATTCGCGAGTGGGTTCCGCTCTCGTCCGATCTATCGCGGCGCAGCGGCGCGGTGC 1440
 Db 1475 CGTATTCGCGAGTGGGTTCCGCTCTCGTCCGATCTATCGCGGCGCAGCGGCGCGGTGC 1534

QY 1441 CCGGACCGCGTGGATCGTTTCGTAGTACCCGAGAGCTTTGAGAGCTTAAGGCAATTGGG 1500
 Db 1535 CCGGACCGCGTGGATCGTTTCGTAGTACCCGAGAGCTTTGAGAGCTTAAGGCAATTGGG 1594
 QY 1501 AAGATACCTTGGACCTTTCCCATCAATAGAGGAAAAAGCATCGCCCTAGGGGATCCGTAGCGG 1560
 Db 1595 AAGATACCTTGGACCTTTCCCATCAATAGAGGAAAAAGCATCGCCCTAGGGGATCCGTAGCGG 1654
 QY 1561 GCGCGTGTTCAGTGAACCTTGGGAGGGCAATCCCATCGCGCGCAGCGCGGAGCGG 1620
 Db 1655 GCGCGTGTTCAGTGAACCTTGGGAGGGCAATCCCATCGCGCGCAGCGCGGAGCGG 1714
 QY 1621 AAATCCAGGATCCCATCACCATCACCATCACTGA 1655
 Db 1715 AAATCCAGGATCCCATCACCATCACCATCACTGA 1749

RESULT 2
 US-09-351-348-58
 ; Sequence 58, Application US/09351348
 ; Patent No. 6436898
 ; GENERAL INFORMATION:
 ; APPLICANT: Delcayre, Alain
 ; TITLE OF INVENTION: Compounds and Methods for the Treatment
 ; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
 ; FILE REFERENCE: 11000.1042
 ; CURRENT APPLICATION NUMBER: US/09/351,348
 ; CURRENT FILING DATE: 1999-07-12
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 58
 ; LENGTH: 1749
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-351-348-58

Query Match 100.0%; Score 1655; DB 3; Length 1749;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATCTATCTACTCGACCTTCGCGGCGTACCCGGGTGGCTTGAAGTACTCCGGCC 60
 Db 95 GATCTATCTACTCGACCTTCGCGGCGTACCCGGGTGGCTTGAAGTACTCCGGCC 154
 QY 61 ATCCGCTGGCGACCGGCTTCGCGGCTCGCAGCATCAACGCGATGGAAGACGAAGCATGG 120
 Db 155 ATCCGCTGGCGACCGGCTTCGCGGCTCGCAGCATCAACGCGATGGAAGACGAAGCATGG 214
 QY 121 TGGCCAAACGCTCCCGCATCGGCGAGCGGTCTCGGACCGGGTCTCGCGGATCTCGCGG 180
 Db 215 TGGCCAAACGCTCCCGCATCGGCGAGCGGTCTCGGACCGGGTCTCGCGGATCTCGCGG 274
 QY 181 CCGCGCACCTTCGCTCGGCGAAGTCCCGGCGCTCGGCGTCTTTGCGGCGGGATCTGATC 240
 Db 275 CCGCGCACCTTCGCTCGGCGAAGTCCCGGCGCTCGGCGTCTTTGCGGCGGGATCTGATC 334
 QY 241 CAGAACCGGCGCGGTTCGCGGGTTGAGTCTCTCGGTCCCGAGTCCGTCGACGCGAGCTCG 300
 Db 335 CAGAACCGGCGCGGTTCGCGGGTTGAGTCTCTCGGTCCCGAGTCCGTCGACGCGAGCTCG 394
 QY 301 TCGCGGCTGTGATCGGCGCGGCTCGGTAGGCGTCTCGGTCCCAACGTCAGACCGGTGCC 360
 Db 395 TCGCGGCTGTGATCGGCGCGGCTCGGTAGGCGTCTCGGTCCCAACGTCAGACCGGTGCC 454
 QY 361 GGGCGGATGGATCTATCAGTTTCGGCTTCGCGGCGGCGGAGGCGGAGCTTCGG 420
 Db 455 GGGCGGATGGATCTATCAGTTTCGGCTTCGCGGCGGCGGAGGCGGAGCTTCGG 514
 QY 421 CTCGCGGCTGATCGGGTTGGGTTCGTCGCGGCGAGCAGCAGCATCCACCGGAGTCCA 480
 Db 515 CTCGCGGCTGATCGGGTTGGGTTCGTCGCGGCGAGCAGCAGCATCCACCGGAGTCCA 574

481 GMAACGGTCCCGACGGTGCACATCTCCAGTCCGATGAAACGCGGAGCTCGGGACGT 540
Db |
575 GCAACGGGTCCCGACGGTGCACATCTCCAGTCCGATGAAACGCGGAGCTCGGGACGT 634
Qy |
541 CGCGGGCAGCAGCAGCTTTGTTTCAGATGGCAGTCCGCGTGCATGATCCCGGGTTGGCGT 600
Db |
635 CGCGGGCAGCAGCAGCTTTGTTTCAGATGGCAGTCCGCGTGCATGATCCCGGGTTGGCGT 694
Qy |
601 CFTCGGGCTCGCGGATCCAGCAGTCCGCGAGGACATGACACCGGAGCAAGCTCGG 660
Db |
695 CGTCCGGCTCGCGGATCCAGCAGTCCGCGAGGACATGACACCGGAGCAAGCTCGG 754
Qy |
661 GCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db |
755 GCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 814
Qy |
721 GAGACCGGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db |
815 GAGACCGGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 874
Qy |
781 CCGCGAACCGGTTCGAGTGCACCCCGGGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db |
875 CCGCGAACCGGTTCGAGTGCACCCCGGGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 934
Qy |
841 CACGGATGATCTGATCGGAGGATCAGACAGTAAAGCGGTTCGGTTGAATCCA 900
Db |
935 CACGGATGATCTGATCGGAGGATCAGACAGTAAAGCGGTTCGGTTGAATCCA 994
Qy |
901 ATGTGCTGTCAGCAGGATCCGATGCGGAACCGGACCGGACCGGACCGGACCGGACCGGAC 960
Db |
995 ATGTGCTGTCAGCAGGATCCGATGCGGAACCGGACCGGACCGGACCGGACCGGACCGGAC 1054
Qy |
961 TCAGCAGCCCTGGGTTCACCGGGCGTGTGCTTCGCAACCGGACCGGACCGGACCGGACCGG 1020
Db |
1055 TCAGCAGCCCTGGGTTCACCGGGCGTGTGCTTCGCAACCGGACCGGACCGGACCGGACCGG 1114
Qy |
1021 CCGTGGCGCGGCTCTCCATGAGCGGTTCGTTGAGTCCGTCGCTCCGTTGGCTGTTCTGC 1080
Db |
1115 CCGTGGCGCGGCTCTCCATGAGCGGTTCGTTGAGTCCGTCGCTCCGTTGGCTGTTCTGC 1174
Qy |
1081 GAACGGGCGCGGCGGCTCTCCATGAGCGGTTCGTTGAGTCCGTCGCTCCGTTGGCTGTTCTGC 1140
Db |
1175 GAACGGGCGCGGCGGCTCTCCATGAGCGGTTCGTTGAGTCCGTCGCTCCGTTGGCTGTTCTGC 1234
Qy |
1141 CAGCGGTACTTTGCGCCCGAGAACAGCGGTTCGCTCGCGGACCGGACCGGACCGGACCGG 1200
Db |
1235 CAGCGGTACTTTGCGCCCGAGAACAGCGGTTCGCTCGCGGACCGGACCGGACCGGACCGG 1294
Qy |
1201 GCGAGATACACCGAGGCGGTGGCGGATGTCAGATGTCGCGGACCGGACCGGACCGGACCGG 1260
Db |
1295 GCGAGATACACCGAGGCGGTGGCGGATGTCAGATGTCGCGGACCGGACCGGACCGGACCGG 1354
Qy |
1261 TGGAGATCGGATCTATCGCGGCTGTGCGGAGGACGAGGCGGTAGCGGCGGTTCGACT 1320
Db |
1355 TGGAGATCGGATCTATCGCGGCTGTGCGGAGGACGAGGCGGTAGCGGCGGTTCGACT 1414
Qy |
1321 ACGTGCGCCCGGTTGGCGAGAGCAGGATCATCGACCGGACCGGACCGGACCGGACCGG 1380
Db |
1415 ACGTGCGCCCGGTTGGCGAGAGCAGGATCATCGACCGGACCGGACCGGACCGGACCGG 1474
Qy |
1381 CGTATCGCGAGTTCGCTTCGTCAGTACCGGAGCTCTTTCAGAGCTTAAGGCCAATTTGGG 1440
Db |
1475 CGTATCGCGAGTTCGCTTCGTCAGTACCGGAGCTCTTTCAGAGCTTAAGGCCAATTTGGG 1534
Qy |
1441 CCGGACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db |
1535 CCGGACCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1594
Qy |
1501 AAGATCTTGGACCTTCCCATCAATAGAGGAAAGCATCGCCCTTAGGGGATTCGCTAGCGG 1560
Db |
1595 AAGATCTTGGACCTTCCCATCAATAGAGGAAAGCATCGCCCTTAGGGGATTCGCTAGCGG 1654

Qy 1561 GCCCGGTGTTTCGATGAACTTGGCGAGGCAATCCCATCGCGCGCAGCCCGCAGCGG 1620
Db |
1655 GCCCGGTGTTTCGATGAACTTGGCGAGGCAATCCCATCGCGCGCAGCCCGCAGCGG 1714
Qy 1621 AAATCCAGGATCCCATCACCATCACCATCACTGA 1655
Db 1715 AAATCCAGGATCCCATCACCATCACCATCACTGA 1749

RESULT 3
US-09-450-072-56
; Sequence 56, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder:
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-450-072-56

Query Match 61.1%; Score 1011.4; DB 3; Length 1749;
Best Local Similarity 78.9%; Pred. No. 3.5e-213;
Matches 1329; Conservative 0; Mismatches 296; Indels 60; Gaps 8;

Qy 1 GATCTATCTACTCGACCTTTCGCGGACCGGGGTGACCCGGGTGGCTGTGAGTACTCGGCG 60
Db 95 GATCTATCTACTCGACCTTTCGCGGACCGGGGTGACCCGGGTGGCTGTGAGTACTCGGCG 154
Qy 61 ATCCGCTGGCGACCGGCTCGCGGTTCGCGAGCATCAACCGATGGAAGAGCAAGGATGG 120
Db 155 ATCCGCTGGCGACCGGCTCGCGGTTCGCGAGCATCAACCGATGGAAGAGCAAGGATGG 214
Qy 121 TGSCCAACCGCTGCCCATTCGCGAGCAGGTCTCGGAACCGGTCTGCGCGATCTCGCG 180
Db 215 TGSCCAACCGCTGCCCATTCGCGAGCAGGTCTCGGAACCGGTCTGCGCGATCTCGCG 274
Qy 181 CCGGACACCGTTTCGCTCGCGGAGTCCGCGGCTTCGCGGTCTTCGCGGCGGATCTGATC 240
Db 275 CCGGACACCGTTTCGCTCGCGGAGTCCGCGGCTTCGCGGTCTTCGCGGCGGATCTGATC 334
Qy 241 CAGAACCGGCGGTCTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 300
Db 335 CAGAACCGGCGGTCTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCG 394
Qy 301 TCSCGCGCTGTGATGCGCGCGCTGAGGGCTCTCGGTTCGCAACACGTCAGCACCGTCC 360
Db 395 TCSCGCGCTGTGATGCGCGCGCTGAGGGCTCTCGGTTCGCAACACGTCAGCACCGTCC 454
Qy 361 GCGCGGATGATCTATCAGTTTCGCGGCTTCGCGGCTTCGCGGCTTCGCGGCTTCGCGG 420
Db 455 GCGCGGATGATCTATCAGTTTCGCGGCTTCGCGGCTTCGCGGCTTCGCGGCTTCGCGG 510
Qy 421 CTCGCGGCTGATCGGGTTGGGTTCGCTCGGCGGCGGACACAGCATCCACCGAGGTGGA 480
Db 511 TCCAATGTGTGTGTCAGCAGGATCCGA-----TGCGGAACACCGACCGAGGAGTGC 564
Qy 481 GCAACGGTCCCGAGCGGTGACATCTCCAGTTCGATGAAACCGCGCGAGTCTCGGGGAG 540
Db 565 GCAATGTGTTCGCGACCTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCGGTTCGCG 624
Qy 541 CCGCGCGCAGCAGCAGCTTGTTCAGATGGCAGTTCGCGGTTCGATTCGCGGTTCGCGGT 600

QY 661 GCCTGGGATCTGATCAGCTCGGGAGCCGGGTGCCAGCAACCCAGCGTGGGAAGCACC 720
 Db 617 GCCTGGGATCTGATC-----GGCAGGATCAAGACAGTAAAGCGGTTCCTGGTT 666
 QY 721 GAGACCGGCGGATGTGCGCGCAGCAGCGCCAGCGGTGCACCCCGGGAGACCGGGCC 780
 Db 667 GAATCCNATGTGTTCAGCAGGATCCGATGCGAACCAGCAGCGAGAGTCCGA 726
 QY 781 CCGCGGACCGGTTCGAGTCCAGCCCGGCGCCACCGCGCGCGGTGTGTCAGCATCAGC 840
 Db 727 ATCTGTCTCCGACCCCTGGCGTCAAGCGGGTCTGGTCTCCGCAACCGCGCGCATGTC 786
 QY 841 CAGCGGATGATCTGATCCGACGC---ATCAGCAACAGTAAGCGGTGTTCGGTTGAT 897
 Db 787 GCCTGGCGGCTCGCGCGGCTCTCCATGCGCGGTTCGTTCACTGCTGTCGCGGTGGT 846
 QY 898 CCAATGTGCTCAGCAGGATCCGATGCGCAACACCGACCGCAGCAGTCCGAATCT 957
 Db 847 GTTCGGAACGGCGCGCGCGCTGCTGCTCGATACGGGATCTGATCAGCTCGGG 906
 QY 958 GTCTCGGACCTTGGGTCAAGCGGGTCTGTGCTTCGCAACCCCGCGGAGATGTCCGCG 1017
 Db 907 GAGCGGGTCCCAAGCAACCGCAGCGGTGGGAACACCGAGACCGGGCGATGTGCCCGG 966
 QY 1018 GCGCGCTGCGGCGGCTCTCCATGCGCGGTTCGTTCACTGCTGCTCGGTGGCTGTT 1077
 Db 967 CAGCAGCGCCAGCGGTGCAACCCCGCGGACCGGGCCCGCGACCGGTTCGAGTCCGAC 1026
 QY 1078 TGGCAACGGGCGCGCGCGCC-----CGTCTGCTCGTCCGATACGGGATCTATCAGCAG 1130
 Db 1027 CCGGCGCGCACCGCGCGCGGTGTGTCAGCATCAGCCAGCGGATGATCTATCAGCAG 1086
 QY 1131 GTAGGCGCTCCAGCGTACTCTTCGCGCCAGAAACAGCGGTGCGTCCGCGCGCAGACCG 1190
 Db 1087 GTAGGCGCTCCAGCGTACTCTTCGCGCCAGAAACAGCGGTGCGTCCGCGCGCAGACCG 1146
 QY 1191 CGGTCTGCGCGCAGATACACCCAGCGGTGGCGCGCATGTCCAGATCGTGGCCAGCGG 1250
 Db 1147 CGGTCTGCGCGCAGATACACCCAGCGGTGGCGCGCATGTCCAGATCGTGGCCAGCGG 1206
 QY 1251 CCGGCGACGCTGAGATCGGATCTATCGCGCGCTGTGCGGGAAGACAGGCGCTAGCG 1310
 Db 1207 CCGGCGACGCTGAGATCGGATCTATCGCGCGCTGTGCGGGAAGACAGGCGCTAGCG 1266
 QY 1311 GCGTTGCACTACGTGCGCGCGGTGGCGAAGAGGACTACATCGACGAGCGCTTGGCG 1370
 Db 1267 GCGTTGCACTACGTGCGCGCGGTGGCGAAGAGGACTACATCGACGAGCGCTTGGCG 1326
 QY 1371 AACATCGGCGCGTATCTGCCAGCTGAGGTTCCCGCTCTCGTCG----- 1413
 Db 1327 AACATCGGCGCGTATCTGCCAGCTGAGGTTCCCGCTCTCGTCGATCTGATCAGAACGG 1386
 QY 1414 ----- 1413
 Db 1387 GCGGCTCTCGGTTGAGGTCTCTCGGTGCCAGTGCCTGCGACGCGAGCGTCTGCGGCT 1446
 QY 1414 ----- 1413
 Db 1447 GGTGATGCGCGCGCTGAGGCTCTCTCGGTCCAAACGTGAGCAGCGTCCCGGGGGAT 1506
 QY 1414 -GATCTATCGCGCACCGCGCGGTGCGCGGACCGCGTGGATCGTTGTCAGTACCGG 1472
 Db 1507 GGATCTATCGCGCGCACCGCGCGGTGCGCGGACCGCGTGGATCGTTGTCAGTACCGG 1566
 QY 1473 AAGCTCTGAGAGCTAAGGCAATTTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAA 1532
 Db 1567 AAGCTCTGAGAGCTAAGGCAATTTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAA 1626
 QY 1533 AAGCATCGCCTAGGGGATCCGTAGCGGGCGCGGTGTTTCAGTGAACCTTGGCGAGGCA 1592
 Db 1627 AAGCATCGCCTAGGGGATCCGTAGCGGGCGCGGTGTTTCAGTGAACCTTGGCGAGGCA 1686

QY 1593 ATCCCATCGCGCAGCGCGCGGAAATCCACGATCCCATCACCATCACCATCACCATC 1652
 Db 1687 ATCCCATCGCGCAGCGCGCGGAAATCCACGATCCCATCACCATCACCATCACCATC 1746
 QY 1653 TGA 1655
 Db 1747 TGA 1749
 RESULT 6
 US-09-351-348-57
 ; Sequence 57, Application US/09351348
 ; Patent No. 6436898
 ; GENERAL INFORMATION:
 ; APPLICANT: Delcayre, Alain
 ; TITLE OF INVENTION: Compounds and Methods for the Treatment
 ; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
 ; FILE REFERENCE: 11000.1042
 ; CURRENT APPLICATION NUMBER: US/09/351,348
 ; CURRENT FILING DATE: 1999-07-12
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 57
 ; LENGTH: 1749
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Made in a lab
 US-09-351-348-57
 Query Match 44.7%; Score 740.2; DB 3; Length 1749;
 Best Local Similarity 69.0%; Pred. No. 1.5e-153;
 Matches 1244; Conservative 0; Mismatches 263; Indels 296; Gaps 5;
 QY 1 GATCTATCTACTCGACCTTTCGCGCAGCGGGCGTACCCGGGTGCTGAGTACTCGGCG 60
 Db 95 GATCTATCTACTCGACCTTTCGCGCAGCGGGCGTACCCGGGTGCTGAGTACTCGGCG 154
 QY 61 ATCCGCTGGCGACCGCTCGCGGTGCGGACCATCAACCGGATGGAAGAGGATCG 120
 Db 155 ATCCGCTGGCGACCGCTCGCGGTGCGGACCATCAACCGGATGGAAGAGGATCG 214
 QY 121 TGGCCAAACCTCGCCGATCGCGAGCAGGTGCTCGGACCGGCTCTGCGCGATCTCGCG 180
 Db 215 TGGCCAAACCTCGCCGATCGCGAGCAGGTGCTCGGACCGGCTCTGCGCGATCTCGCG 274
 QY 181 CCGCGCACCTTTCGCTCGCGAAGTCCGCGCTCGGCGTCTTCTGGGCGGGATCTGATC 240
 Db 275 CCGCGCACCTTTCGCTCGCGAAGTCCGCGCTCGGCGTCTTCTGGGCG----- 324
 QY 241 CAGAACGGGCGGCTCTGCGGTTGAGGTCTCTCGGTGCCAGTGCCTCGACGCGATCG 300
 Db 325 ----- 324
 QY 301 TCGGCGCTGATGATGCGCGCGGTAGGCGTCTCTCGGTCCAAACGTGAGCAGCGTCC 360
 Db 325 ----- 324
 QY 361 GGGCGGATGATCTATCTATCTGCGGCTTGGTCCGACGCGCGCGGAGGCGAGTCCG 420
 Db 325 -----GGATCTATCTGCTGCGGCTTGGTCCGACGCGCGCGGAGGCGAGTCCG 376
 QY 421 CTCGCGCTGATCGGTTGGGTTCGTCGCGGCGCAGCACACGATCCACCGAGTCCGA 480
 Db 377 CTCGCGCTGATCGGTTGGGTTCGTCGCGGCGCAGCACACGATCCACCGAGTCCGA 436
 QY 481 GCAACGGGTCGCCGAGTGCATCTCCAGTTCGATGAACCGCGAGCTCGGGGACGT 540
 Db 437 GCAACGGGTCGCCGAGTGCATCTCCAGTTCGATGAACCGCGAGCTCGGGGACGT 496
 QY 541 CCGCGCGCAGCAGCTTGTTCAGATGCGAGTCCGCGTGCATGATCCCGGGTTCGGCGT 600
 Db 497 CCGCGCGCAGCAGCTTGTTCAGATGCGAGTCCGCGTGCATGATCCCGGGTTCGGCGT 556

```
QY 601 CGTGGGCTTGGCGAGTCCAGCAGTCCGCGAGCACATGACCCGACGGGAACGACTCCG 660
Db 557 CTTGGGCGCTTGGCGAGTCCAGCAGTCCGCGAGCACATGACCCGACGGGAACGACTCCG 616
QY 661 GCGCGGATCTGATCAGTCCGCGAGCCGCGTCCAGCAACGCCAGCTGGGAAGCAC 720
Db 617 GCGCGGATCTGATC-----GCGAGCATCACGAACAGTAAGCGGTTCGGTT 666
QY 721 GAGACCGCGCGATGTGCGCGCAGCAGCGCCAGCGCTGTCACCCGCGGGACCGGCG 780
Db 667 GATCCAAATGTGTGTGTCAGCAGCATCCGATGCCGAACACCGACACGCGAGCAGTCGCA 726
QY 781 CCGCGGACCGCTGCGAGTCCAGCCCGCGCCGCGCACCGCGCGCGTGTGTCAGCATCAGC 840
Db 727 ATCTGTCTCCGACCTTGGGTCTCATGTCGCGGTCTGTGCTCCGCAACCCGCGCGATGTC 786
QY 841 CACGGATGATCTGATCCGACGC---ATCACGAACAGTAAGCGGTGTTCGGTTGAAT 897
Db 787 GCGCGCGCGCTCGCGCGCTCTCCATGTCGCGTTCGTTCACTGCTGTCGCGTGGCT 846
QY 898 CCAATGTGTGTCAGCAGGATCCGATGCCGAACACCGACACCGCAGCAGTCCGCAATCT 957
Db 847 GTTCTCGAAGCGCGCGCGCGCTCTCCATGTCGCTCCGTCGATACGGGATCTGATCAGCTCGG 906
QY 958 GTCTCGGACCTTGGGTTCAGCGCGCGTCTGTGCTCCGCAACCCGCGCGATGTCGCGC 1017
Db 907 GAGCGGCTCCAGCAACCCAGCTGGAAGAACCGAGACCGCGCGATGTCGCGCG 966
QY 1018 GCGCGCTGCGCGCGCTCTCCATGTCGCGGTCTGTTCAGTCTGCTGCTGCGTGGCTGTT 1077
Db 967 CAGCAGCGCCAGCGTGACCCCGCGGACCGGCGCCCGCGACCGCTGCGAGTCGAC 1026
QY 1078 TGGGAACGGCGCCCGCGCGC-----CGTCTGCTCCGATACGGGATCTATCAGCAG 1130
Db 1027 CCGCGCGCACCGCGCGCGTGTGTGATCAGCATCAGCACCGGATGATCTATCAGCAG 1086
QY 1131 GTAGCGCTCCAGCGTACTTTCGCGCCAGAACAGCGGTGCGTCCGCGCAGACCCAG 1190
Db 1087 GTAGCGCTCCAGCGTACTTTCGCGCCAGAACAGCGGTGCGTCCGCGCAGACCCAG 1146
QY 1191 CGGTCTTCCGCGCAGATACACCCAGCGGTGCGCGCATGTCCAGATCTGTGGCCAGCGG 1250
Db 1147 CGGTCTTCCGCGCAGATACACCCAGCGGTGCGCGCATGTCCAGATCTGTGGCCAGCGG 1206
QY 1251 CCGCGCACGCTGAGATCGATCTATCGCGCGCTGTGCGGGAAGGAGCGCGCTAGCG 1310
Db 1207 CCGCGCACGCTGAGATCGATCTATCGCGCGCTGTGCGGGAAGGAGCGCGCTAGCG 1266
QY 1311 GCGTTGCACTACGTCGCGCGGTGCGGAGAGCAGGACTACATCGACCGAGCTTGC 1370
Db 1267 GCGTTGCACTACGTCGCGCGGTGCGGAGAGCAGGACTACATCGACCGAGCTTGC 1326
QY 1371 AACATCGGCGCTATCTGCCAGCTGAGGTTCCCGCTCTCGTCG----- 1413
Db 1327 AACATCGGCGCTATCTGCCAGCTGAGGTTCCCGCTCTCGTCGATCTGATCCAGACGG 1386
QY 1414 ----- 1413
Db 1387 GCGGCTCTCGGGTTGAGTCTCTCGGTGCCAGTCCGCTGACCGGACGTCGTGCGGCT 1446
QY 1414 ----- 1413
Db 1447 GGTGATCGCGCGCGTAGCGTCTCTCGGTCCAAACGTACGACCGTGGCGCGCGAT 1506
QY 1414 -GATCTATCGCGCACCGCGCGCTGCGCGCACCGCGTGGATCTGTCTGTCAGTACCGG 1472
Db 1507 GATCTATCGCGCACCGCGCGCTGCGCGCACCGCGTGGATCTGTCTGTCAGTACCGG 1566
QY 1473 AAGCTCTTGAGAGCTAAGGCGCAATTGGGAAGATATTGGACCTTCCCATCAATAGAGAA 1532
Db 1567 AAGCTCTTGAGAGCTAAGGCGCAATTGGGAAGATATTGGACCTTCCCATCAATAGAGAA 1626
```

```
QY 1533 AAGCATCGCCCTAGGGATCCGTAGCGGCGCGGTGTTTCGATGTAACTTGGGCGGGCA 1592
Db 1627 AAGCATCGCCCTAGGGATCCGTAGCGGCGCGGTGTTTCGATGTAACTTGGGCGGGCA 1686
QY 1593 ATCCCATCGCGCGCAGCGCGCGGGAATCCACGGATCCATCACCATCACCATCAC 1652
Db 1687 ATCCCATCGCGCGCAGCGCGCGGGAATCCACGGATCCATCACCATCACCATCAC 1746
QY 1653 TGA 1655
Db 1747 TGA 1749
```

RESULT 7

```
US-09-450-072-15
; Sequence 15, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-15
```

Query Match 17.6%; Score 291; DB 3; Length 291;

Best Local Similarity 100.0%; Pred. No. 6.3e-55; Mismatches 0; Indels 0; Gaps 0;

Matches 291; Conservative 0;

```
QY 375 ATCAGTTCCGGCCCTGCTGCGCAGCCGCGAGGCGAGCCAGATTCGCTCCGGGTTCGATC 434
Db 1 ATCAGTTCCGGCCCTGCTGCGCAGCCGCGAGGCGAGCCAGATTCGCTCCGGGTTCGATC 60
QY 435 GGGTTGGGTTCGCTCCGGCCAGCACACAGCATCCACCCGAGGTTCGAGCAACGGGTTCGCG 494
Db 61 GGGTTGGGTTCGCTCCGGCCAGCACACAGCATCCACCCGAGGTTCGAGCAACGGGTTCGCG 120
QY 495 ACGGTGCACATCTCCAGTCGATGAACGCGCGAGCTCGGGAGCTCGCGCGCAGCAGC 554
Db 121 ACGGTGCACATCTCCAGTCGATGAACGCGCGAGCTCGGGAGCTCGCGCGCAGCAGC 180
QY 555 ACGTTGTCAGATGGCAGTCGCGCTGCATGATCCCGGTTTCGGGCTTCGGGCTTCGCG 614
Db 181 ACGTTGTCAGATGGCAGTCGCGCTGCATGATCCCGGTTTCGGGCTTCGGGCTTCGCG 240
QY 615 GAGTCCAGCCAGTCGCGGAGCACATGCACCGAGGGAACGACTCGGGCGCG 665
Db 241 GAGTCCAGCCAGTCGCGGAGCACATGCACCGAGGGAACGACTCGGGCGCG 291
```

RESULT 8

```
US-09-351-348-15
; Sequence 15, Application US/09351348
; Patent No. 643698
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
```



```
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-351-348-15

Query Match      17.6%; Score 291; DB 3; Length 291;
Best Local Similarity 100.0%; Pred. No. 6.3e-55;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 ATCAGTTGGCCCTGTGTCGACGCCCGGAGGCGACGATTCCTCGGCGTGCATC 434
Db 1 ATCAGTTGGCCCTGTGTCGACGCCCGGAGGCGACGATTCCTCGGCGTGCATC 60

QY 435 GGGTTCGGTCCGTCGGCCAGCACACGAGCATCCACCGGAGTTCGAGCAACGGTCCCG 494
Db 61 GGGTTCGGTCCGTCGGCCAGCACACGAGCATCCACCGGAGTTCGAGCAACGGTCCCG 120

QY 495 ACGGTGCACATCTCCAGTCGATGAACCGCGCGAGCTCGGGGACGTTCGGGCGCAGCAGC 554
Db 121 ACGGTGCACATCTCCAGTCGATGAACCGCGCGAGCTCGGGGACGTTCGGGCGCAGCAGC 180

QY 555 ACCTTGTTCAGATGGCAGTCCCGTCGATGATCCCGGGTTCGGCGTTCGGGCGCTGCGC 614
Db 181 ACCTTGTTCAGATGGCAGTCCCGTCGATGATCCCGGGTTCGGCGTTCGGGCGCTGCGC 240

QY 615 GAGTCCAGCCAGTCCGGGAGCACATGCACCGCGGAAACGACTTCGGGCGG 665
Db 241 GAGTCCAGCCAGTCCGGGAGCACATGCACCGCGGAAACGACTTCGGGCGG 291

RESULT 9
US-09-450-072-18
; Sequence 18, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-18

Query Match      15.8%; Score 261; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.4e-48;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 GATCGCGAGCATCACGAACAGTAAGCGGTGTTCCGGTTGAATCCAAATGTGCTGTGTCAGCA 914
Db 1 GATCGCGAGCATCACGAACAGTAAGCGGTGTTCCGGTTGAATCCAAATGTGCTGTGTCAGCA 60

QY 915 GGCATCCGATGCCGAACACCGACACCGACGAGCAGTGCCTGCTCGGCGCGCGC 974
Db 61 GGCATCCGATGCCGAACACCGACACCGACGAGCAGTGCCTGCTCGGCGCGCGC 120

QY 975 TCACGCGCGCTGTGGCTCCGCAACCCCGCGCGATGTCCGCGCGCGCTGCGGCGCGC 1034
Db 121 TCACGCGCGCTGTGGCTCCGCAACCCCGCGCGATGTCCGCGCGCGCTGCGGCGCGC 180

QY 1035 TCTCCATGCGCGGTTCGTTCAATGCTGCTCGGTTGGTGTCTGCGAACGGGCCCGCG 1094
Db 181 TCTCCATGCGCGGTTCGTTCAATGCTGCTCGGTTGGTGTCTGCGAACGGGCCCGCG 240

QY 1095 CCCCCTGCTCCGTCGCGATACG 1115
Db 241 CCCCCTGCTCCGTCGCGATACG 261

RESULT 11
US-09-450-072-14
; Sequence 14, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 697
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-14

Query Match      13.7%; Score 226; DB 3; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATCTACTCGACCTTCGCGCGGCGTACCCGGGTGGCTGACGTACTCCGGGCATCCG 65
```

```
Db 241 CCCCCTGCTCCGTCGCGATACG 261

RESULT 10
US-09-351-348-18
; Sequence 18, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-351-348-18

Query Match      15.8%; Score 261; DB 3; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.4e-48;
Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 855 GATCGCGAGCATCACGAACAGTAAGCGGTGTTCCGGTTGAATCCAAATGTGCTGTGTCAGCA 914
Db 1 GATCGCGAGCATCACGAACAGTAAGCGGTGTTCCGGTTGAATCCAAATGTGCTGTGTCAGCA 60

QY 915 GGCATCCGATGCCGAACACCGACACCGACGAGCAGTGCCTGCTCGGCGCGCGC 974
Db 61 GGCATCCGATGCCGAACACCGACACCGACGAGCAGTGCCTGCTCGGCGCGCGC 120

QY 975 TCACGCGCGCTGTGGCTCCGCAACCCCGCGCGATGTCCGCGCGCGCTGCGGCGCGC 1034
Db 121 TCACGCGCGCTGTGGCTCCGCAACCCCGCGCGATGTCCGCGCGCGCTGCGGCGCGC 180

QY 1035 TCTCCATGCGCGGTTCGTTCAATGCTGCTCGGTTGGTGTCTGCGAACGGGCCCGCG 1094
Db 181 TCTCCATGCGCGGTTCGTTCAATGCTGCTCGGTTGGTGTCTGCGAACGGGCCCGCG 240

QY 1095 CCCCCTGCTCCGTCGCGATACG 1115
Db 241 CCCCCTGCTCCGTCGCGATACG 261

RESULT 11
US-09-450-072-14
; Sequence 14, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 697
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-14

Query Match      13.7%; Score 226; DB 3; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATCTACTCGACCTTCGCGCGGCGTACCCGGGTGGCTGACGTACTCCGGGCATCCG 65
```


Db 1 ATCTACTCGACCTTCGCGGACCGGGGTACCCCGGGTGGCCCTGACGTACTCCGSCCATCCG 60
Qy 66 CTGGCGACCGCCTTCGCGGCTCGGACGATCAACGCGGATGGAAGACGAGCATGTGGCC 125
Db 61 CTGGCGACCGCCTTCGCGGCTCGGACGATCAACGCGGATGGAAGACGAGCATGTGGCC 120
Qy 126 AACGCTGCCCGCATCGCGAGCAGGTCTCGGACCGGGTCTGCGCGATCTCGCGCCCGG 185
Db 121 AACGCTGCCCGCATCGCGAGCAGGTCTCGGACCGGGTCTGCGCGATCTCGCGCCCGG 180
Qy 186 CACCGTTTCGGTTCGCGGAAGTCCGCGCTCGGGTCTTCCTGGCGG 231
Db 181 CACCGTTTCGGTTCGCGGAAGTCCGCGCTCGGGTCTTCCTGGCGG 226

RESULT 12
US-09-351-348-14
; Sequence 14, Application US/09351348
; Patent No. 643688
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 697
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-351-348-14

Query Match 13.7%; Score 226; DB 3; Length 697;
Best Local Similarity 100.0%; Pred. No. 1.5e-40;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 ATCTACTCGACCTTCGCGGACCGGGGTACCCCGGGTGGCCCTGACGTACTCCGSCCATCCG 65
Db 1 ATCTACTCGACCTTCGCGGACCGGGGTACCCCGGGTGGCCCTGACGTACTCCGSCCATCCG 60
Qy 66 CTGGCGACCGCCTTCGCGGCTCGGACGATCAACGCGGATGGAAGACGAGCATGTGGCC 125
Db 61 CTGGCGACCGCCTTCGCGGCTCGGACGATCAACGCGGATGGAAGACGAGCATGTGGCC 120
Qy 126 AACGCTGCCCGCATCGCGAGCAGGTCTCGGACCGGGTCTGCGCGATCTCGCGCCCGG 185
Db 121 AACGCTGCCCGCATCGCGAGCAGGTCTCGGACCGGGTCTGCGCGATCTCGCGCCCGG 180
Qy 186 CACCGTTTCGGTTCGCGGAAGTCCGCGCTCGGGTCTTCCTGGCGG 231
Db 181 CACCGTTTCGGTTCGCGGAAGTCCGCGCTCGGGTCTTCCTGGCGG 226

RESULT 13
US-09-450-072-13
; Sequence 13, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 210

; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-13
Query Match 12.7%; Score 210; DB 3; Length 210;
Best Local Similarity 100.0%; Pred. No. 3.8e-37;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1419 ATCGCGCCACCGCGCGGTGCCCGCACCGCGTGGATCGTTCGTCAGTACCCGGAAGCTC 1478
Db 1 ATCGCGCCACCGCGCGGTGCCCGCACCGCGTGGATCGTTCGTCAGTACCCGGAAGCTC 60
Qy 1479 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAAAGCAT 1538
Db 61 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAAAGCAT 120
Qy 1539 CGCCCTAGGGGATCCGTAGCGGGCCCGGTTCGTGAGTGAACCTTGGGCGGCAATCCCA 1598
Db 121 CGCCCTAGGGGATCCGTAGCGGGCCCGGTTCGTGAGTGAACCTTGGGCGGCAATCCCA 180
Qy 1599 TCGCGCGCAGCCCGCGCAGCGGAATCCAC 1628
Db 181 TCGCGCGCAGCCCGCGCAGCGGAATCCAC 210

RESULT 14
US-09-351-348-13
; Sequence 13, Application US/09351348
; Patent No. 643688
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-351-348-13

Query Match 12.7%; Score 210; DB 3; Length 210;
Best Local Similarity 100.0%; Pred. No. 3.8e-37;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1419 ATCGCGCCACCGCGCGGTGCCCGCACCGCGTGGATCGTTCGTCAGTACCCGGAAGCTC 1478
Db 1 ATCGCGCCACCGCGCGGTGCCCGCACCGCGTGGATCGTTCGTCAGTACCCGGAAGCTC 60
Qy 1479 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAAAGCAT 1538
Db 61 TTGAGAGCTAAGGCCCAATTGGGAAGATACTTGGACCTTCCCATCAATAGAGGAAAGCAT 120
Qy 1539 CGCCCTAGGGGATCCGTAGCGGGCCCGGTTCGTGAGTGAACCTTGGGCGGCAATCCCA 1598
Db 121 CGCCCTAGGGGATCCGTAGCGGGCCCGGTTCGTGAGTGAACCTTGGGCGGCAATCCCA 180
Qy 1599 TCGCGCGCAGCCCGCGCAGCGGAATCCAC 1628
Db 181 TCGCGCGCAGCCCGCGCAGCGGAATCCAC 210

RESULT 15
US-09-450-072-21
; Sequence 21, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for Their Use

; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Mycobacterium vaccae
US-09-450-072-21

Query Match 10.7%; Score 177; DB 3; Length 177;
Best Local Similarity 100.0%; Pred.No. 6.7e-30;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

672 GATCAGCTCGGGAGCCGGGTGCCAGCACGCCAGCGTGGGAAGCACCGAGACCGCGC 731
|||||
1 GATCAGCTCGGGAGCCGGGTGCCAGCAACGCCAGCGTGGGAAGCACCGAGACCGCGC 60
|||||
732 GATGTGCCCCCGCAGCAGCGCCCGAGCGGTGCACCCCGCGGACCCGGGCCCCCGCGACCGC 791
|||||
61 GATGTGCCCCCGCAGCAGCGCCCGAGCGGTGCACCCCGCGGACCCGGGCCCCCGCGACCGC 120
|||||
792 GTCGGAGTCGACCCCGGCGCCGACCGCGCGCGTGGTCAGCATCAGCCACGGGAT 848
|||||
121 GTCGGAGTCGACCCCGGCGCCGACCGCGCGCGTGGTCAGCATCAGCCACGGGAT 177
|||||

Search completed: October 7, 2005, 00:30:42
Job time : 316 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: September 16, 2005, 20:35:08 ; Search time 171 Seconds
(without alignments)
1300.031 Million cell updates/sec

Title: US-10-607-752-116
Perfect score: 2862
Sequence: 1 IYSTFADRAYPGGLTYSYGH...IPSRARAAEIHGSHHHHH 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues
Total number of hits satisfying chosen parameters: 1812044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US10H_PUBCOMB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US10I_PUBCOMB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US10J_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2862	100.0	549	15	US-10-607-752-116
2	2862	100.0	582	14	US-10-100-679-81
3	2862	100.0	582	15	US-10-607-752-81
4	2804	98.0	541	14	US-10-100-679-97
5	2804	98.0	541	15	US-10-607-752-97
6	2431	84.9	471	14	US-10-100-679-96
7	2431	84.9	471	15	US-10-607-752-96
8	2184	76.3	423	14	US-10-100-679-95
9	2184	76.3	423	15	US-10-607-752-95
10	2145	74.9	582	14	US-10-100-679-80
11	2145	74.9	582	15	US-10-607-752-80

12	1919	67.1	372	14	US-10-100-679-94
13	1919	67.1	372	15	US-10-607-752-94
14	1906	66.6	582	14	US-10-100-679-79
15	1906	66.6	582	15	US-10-607-752-79
16	1459	51.0	281	14	US-10-100-679-93
17	1459	51.0	281	15	US-10-607-752-93
18	1123	39.2	220	14	US-10-100-679-92
19	1123	39.2	220	15	US-10-607-752-92
20	623	21.8	121	14	US-10-100-679-91
21	623	21.8	121	15	US-10-607-752-91
22	490	17.1	97	14	US-10-100-679-71
23	490	17.1	97	15	US-10-607-752-71
24	440	15.4	87	14	US-10-100-679-74
25	440	15.4	87	15	US-10-607-752-74
26	389	13.6	75	14	US-10-100-679-70
27	389	13.6	75	15	US-10-607-752-70
28	389	13.6	75	15	US-10-607-752-90
29	389	13.6	75	15	US-10-607-752-69
30	373	13.0	70	14	US-10-100-679-69
31	373	13.0	70	15	US-10-607-752-69
32	326	11.4	59	14	US-10-100-679-77
33	326	11.4	59	15	US-10-607-752-77
34	284	9.9	451	14	US-10-156-761-12085
35	255	8.9	49	14	US-10-100-679-72
36	255	8.9	49	15	US-10-607-752-72
37	237	8.3	46	14	US-10-100-679-73
38	237	8.3	46	15	US-10-607-752-73
39	224	7.8	44	14	US-10-100-679-76
40	224	7.8	44	15	US-10-607-752-76
41	220	7.7	445	9	US-09-815-242-11701
42	206	7.2	38	14	US-10-100-679-67
43	206	7.2	38	15	US-10-607-752-67
44	203.5	7.1	19608	15	US-10-084-846A-8
45	197.5	6.9	900	18	US-10-450-763-33892

ALIGNMENTS

RESULT 1
US-10-607-752-116
; Sequence 116, Application US/10607752
; Publication No. US20040072224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder:
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 08/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-607-752-116

Query Match 100.0% Score 2862; DB 15; Length 549;
Best Local Similarity 100.0%; Pred.No. 3.6e-137; Mismatches 0; Indels 0; Gaps 0;
Matches 549; Conservative 0;
QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGVANARIGEQLVGLRLDLAAR 60
DB 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGVANARIGEQLVGLRLDLAAR 60

QY 61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRRRDDVVGAGDAAAVGLGPGQRHRARA 120
Db 61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRRRDDVVGAGDAAAVGLGPGQRHRARA 120
QY 121 DGSISSALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNMAASSGTSR 180
Db 121 DGSISSALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNMAASSGTSR 180
QY 181 RSSTLFRWQSPCMI PGSSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKHRD 240
Db 181 RSSTLFRWQSPCMI PGSSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKHRD 240
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARQOHQPRDGSROASRTVSGVPVSNV 300
Db 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARQOHQPRDGSROASRTVSGVPVSNV 300
QY 301 LSAGIRCRPTTTRAVAI CLATLASGVVAPAGDVVARAAAAGSPWPVRSVARPVAVLRT 360
Db 301 LSAGIRCRPTTTRAVAI CLATLASGVVAPAGDVVARAAAAGSPWPVRSVARPVAVLRT 360
QY 361 GPPRRPSDTGSI TOVGRPAVLFAPEQRCRRRADORSCQIHPPGGRHVQIVASARGTVE 420
Db 361 GPPRRPSDTGSI TOVGRPAVLFAPEQRCRRRADORSCQIHPPGGRHVQIVASARGTVE 420
QY 421 IGSIARLCGDEAVAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
Db 421 IGSIARLCGDEAVAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
QY 481 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 540
Db 481 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 540
QY 541 HGSHHHHH 549
Db 541 HGSHHHHH 549

RESULT 2
US-10-100-679-81
; Sequence 81, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c2
; CURRENT APPLICATION NUMBER: US/10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1998-11-29
; PRIOR APPLICATION NUMBER: 09/361,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-100-679-81

Query Match 100.0%; Score 2862; DB 14; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
Db 34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 93

QY 61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRRRDDVVGAGDAAAVGLGPGQRHRARA 120
Db 94 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRRRDDVVGAGDAAAVGLGPGQRHRARA 153
QY 121 DGSISSALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNMAASSGTSR 180
Db 154 DGSISSALVASPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNMAASSGTSR 213
QY 181 RSSTLFRWQSPCMI PGSSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKHRD 240
Db 214 RSSTLFRWQSPCMI PGSSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKHRD 273
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARQOHQPRDGSROASRTVSGVPVSNV 300
Db 274 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARQOHQPRDGSROASRTVSGVPVSNV 333
QY 301 LSAGIRCRPTTTRAVAI CLATLASGVVAPAGDVVARAAAAGSPWPVRSVARPVAVLRT 360
Db 334 LSAGIRCRPTTTRAVAI CLATLASGVVAPAGDVVARAAAAGSPWPVRSVARPVAVLRT 393
QY 361 GPPRRPSDTGSI TOVGRPAVLFAPEQRCRRRADORSCQIHPPGGRHVQIVASARGTVE 420
Db 394 GPPRRPSDTGSI TOVGRPAVLFAPEQRCRRRADORSCQIHPPGGRHVQIVASARGTVE 453
QY 421 IGSIARLCGDEAVAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
Db 454 IGSIARLCGDEAVAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 513
QY 481 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 540
Db 514 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSRARA AEI 573
QY 541 HGSHHHHH 549
Db 574 HGSHHHHH 582

RESULT 3
US-10-607-752-81
; Sequence 81, Application US/10607752
; Publication No. US20040072224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-05-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1998-11-29
; PRIOR APPLICATION NUMBER: 09/361,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-607-752-81

Query Match 100.0%; Score 2862; DB 15; Length 582;
Best Local Similarity 100.0%; Pred. No. 3.9e-197;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
Db 34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 93
QY 61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRRRDDVVGAGDAAAVGLGPGQRHRARA 120

Db 94 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 153
 QY 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPTVHIISQSMNAASGTSR 180
 Db 154 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPTVHIISQSMNAASGTSR 213
 QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGCEGPAQQRQKHRD 240
 Db 214 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGCEGPAQQRQKHRD 273
 QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHQPDRGSDRQASRTVSGVPVSNV 300
 Db 274 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHQPDRGSDRQASRTVSGVPVSNV 333
 QY 301 LSAGIRCRPTTTRAVAI CLATLASRGVVAPOAGDVVARAAAAGSPWPVRSVARPVAVLRT 360
 Db 334 LSAGIRCRPTTTRAVAI CLATLASRGVVAPOAGDVVARAAAAGSPWPVRSVARPVAVLRT 393
 QY 361 GPPRRPSTGSIITQVGRPAVLFAPEQRCRRADQSCRIHPGGRHVVQIVASARGTVE 420
 Db 394 GPPRRPSTGSIITQVGRPAVLFAPEQRCRRADQSCRIHPGGRHVVQIVASARGTVE 453
 QY 421 IGSIALRCGKDBAVALHYVAPVGEKQYIDRALRNI GPYLPALVGSIAATGPPVPG 480
 Db 454 IGSIALRCGKDBAVALHYVAPVGEKQYIDRALRNI GPYLPALVGSIAATGPPVPG 513
 QY 481 TAWIVRQYPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVFRVNLGRAIPRAARAARI 540
 Db 514 TAWIVRQYPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVFRVNLGRAIPRAARAARI 573
 QY 541 HGSHHHHH 549
 Db 574 HGSHHHHH 582

RESULT 4
 US-10-100-679-97
 ; Sequence 97, Application US/10100679
 ; Publication No. US20030054013A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Delcayre, Alain
 ; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
 ; FILE REFERENCE: 11000.10422
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
 ; PRIOR FILING DATE: 2000-07-10
 ; PRIOR APPLICATION NUMBER: 09/450.072
 ; PRIOR FILING DATE: 1999-11-28
 ; PRIOR APPLICATION NUMBER: 09/451.348
 ; PRIOR FILING DATE: 1999-07-12
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 97
 ; LENGTH: 541
 ; TYPE: PRN
 ; ORGANISM: Mycobacterium vaccae
 US-10-100-679-97

Query Match 98.0%; Score 2804; DB 14; Length 541;
 Best Local Similarity 100.0%; Pred. No. 5.2e-193;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEVLGPGRLDLAAR 60
 Db 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEVLGPGRLDLAAR 60
 QY 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 120
 Db 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 120

QY 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPTVHIISQSMNAASGTSR 180
 Db 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPTVHIISQSMNAASGTSR 180
 QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGCEGPAQQRQKHRD 240
 Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGCEGPAQQRQKHRD 240
 QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHQPDRGSDRQASRTVSGVPVSNV 300
 Db 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHQPDRGSDRQASRTVSGVPVSNV 300
 QY 301 LSAGIRCRPTTTRAVAI CLATLASRGVVAPOAGDVVARAAAAGSPWPVRSVARPVAVLRT 360
 Db 301 LSAGIRCRPTTTRAVAI CLATLASRGVVAPOAGDVVARAAAAGSPWPVRSVARPVAVLRT 360
 QY 361 GPPRRPSTGSIITQVGRPAVLFAPEQRCRRADQSCRIHPGGRHVVQIVASARGTVE 420
 Db 361 GPPRRPSTGSIITQVGRPAVLFAPEQRCRRADQSCRIHPGGRHVVQIVASARGTVE 420
 QY 421 IGSIALRCGKDBAVALHYVAPVGEKQYIDRALRNI GPYLPALVGSIAATGPPVPG 480
 Db 421 IGSIALRCGKDBAVALHYVAPVGEKQYIDRALRNI GPYLPALVGSIAATGPPVPG 480
 QY 481 TAWIVRQYPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVFRVNLGRAIPRAARAARI 540
 Db 481 TAWIVRQYPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVFRVNLGRAIPRAARAARI 540
 QY 541 H 541
 Db 541 H 541

RESULT 5

US-10-607-752-97
 ; Sequence 97, Application US/10607752
 ; Publication No. US20040072224A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Delcayre, Alain
 ; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
 ; FILE REFERENCE: 11000.1042c3
 ; CURRENT FILING DATE: 2003-06-26
 ; PRIOR FILING DATE: 2003-06-26
 ; PRIOR APPLICATION NUMBER: 10/100,679
 ; PRIOR FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 09/450,072
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/451,348
 ; PRIOR FILING DATE: 1999-07-12
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 97
 ; LENGTH: 541
 ; TYPE: PRN
 ; ORGANISM: Mycobacterium vaccae
 US-10-607-752-97

Query Match 98.0%; Score 2804; DB 15; Length 541;
 Best Local Similarity 100.0%; Pred. No. 5.2e-193;
 Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEVLGPGRLDLAAR 60
 Db 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEVLGPGRLDLAAR 60
 QY 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 120
 Db 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 120
 QY 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPTVHIISQSMNAASGTSR 180
 Db 121 DGSISSALVASPPRAASSAPASIGLPGSQHTSIHPRSSNGSPTVHIISQSMNAASGTSR 180

```
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
Db 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
QY 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
QY 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
421 IGSIARLCGKDEAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
421 IGSIARLCGKDEAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
QY 481 TAMIYRQPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVFRVNLGRAIPSAARA AEI 540
Db 481 TAMIYRQPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVFRVNLGRAIPSAARA AEI 540
QY 541 H 541
Db 541 H 541

RESULT 6
US-10-100-679-96
; Sequence 96, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c2
; CURRENT FILING DATE: 2002-03-14
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-100-679-96

Query Match 84.9%; Score 2431; DB 14; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.8e-166;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
Db 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
QY 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGACRRRDVVAGDAAAAGVGLGPQORHARA 120
Db 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGACRRRDVVAGDAAAAGVGLGPQORHARA 120
QY 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
Db 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
Db 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
QY 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
QY 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
421 IGSIARLCGKDEAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
421 IGSIARLCGKDEAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
QY 481 TAMIYRQPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVFRVNLGRAIPSAARA AEI 540
Db 481 TAMIYRQPKLLRAKANWEDTWTFFSIEKHPRGSGVAGPVFRVNLGRAIPSAARA AEI 540
QY 541 H 541
Db 541 H 541

RESULT 7
US-10-607-752-96
; Sequence 96, Application US/10607752
; Publication No. US20040072224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c3
; CURRENT FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2002-03-14
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-607-752-96

Query Match 84.9%; Score 2431; DB 15; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.8e-166;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
Db 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
QY 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGACRRRDVVAGDAAAAGVGLGPQORHARA 120
Db 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGACRRRDVVAGDAAAAGVGLGPQORHARA 120
QY 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
Db 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
Db 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
QY 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
QY 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
```

```
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
Db 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
QY 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
QY 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
421 IGSIARLCGKDEAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGS 471
421 IGSIARLCGKDEAAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGS 471

RESULT 7
US-10-607-752-96
; Sequence 96, Application US/10607752
; Publication No. US20040072224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c3
; CURRENT FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2002-03-14
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-607-752-96

Query Match 84.9%; Score 2431; DB 15; Length 471;
Best Local Similarity 100.0%; Pred. No. 2.8e-166;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
Db 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGLDLAAR 60
QY 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGACRRRDVVAGDAAAAGVGLGPQORHARA 120
Db 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGACRRRDVVAGDAAAAGVGLGPQORHARA 120
QY 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
Db 121 DGSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
Db 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQORQKGRD 240
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
Db 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
QY 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
Db 301 LSAGIRCRTPTTRAVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
QY 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
Db 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRRADORSCROIHPGGGRHVQIVASARGTVE 420
```

Db 361 GPPRRPDSITQVGRPAVLFAPEQRCRRADQSCRQIHPPGGRHVQIVASARGTVE 420
QY 421 IGSIALRCKDRAVAALHVAVPGEKQDYIDRALRNIGPVLPAEVPALVGS 471
Db 421 IGSIALRCKDRAVAALHVAVPGEKQDYIDRALRNIGPVLPAEVPALVGS 471

RESULT 8
US-10-100-679-95
; Sequence 95, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c2
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/NZ00/00121
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-100-679-95

Query Match 76.3%; Score 2184; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.4e-148;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLRDLAAR 60
Db 1 IYSTADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLRDLAAR 60
QY 61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPQORHARA 120
Db 61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPQORHARA 120
QY 121 DGSISSALVAPPPRAASSAPASIGLPGSQHTSIHPRSSNGSPPTVHISQSMNAASSGTSR 180
Db 121 DGSISSALVAPPPRAASSAPASIGLPGSQHTSIHPRSSNGSPPTVHISQSMNAASSGTSR 180
QY 181 RSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEPAQORQKHRD 240
Db 181 RSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEPAQORQKHRD 240
QY 241 RDVPAQQRPAVHPAGPADRVGDPGRHRRARGOHQPRDGSQASRTVSGVPVSNV 300
Db 241 RDVPAQQRPAVHPAGPADRVGDPGRHRRARGOHQPRDGSQASRTVSGVPVSNV 300
QY 301 LSAGIRCRPTTTRAVAICLAATLASRGVVAQPDAGVARAAAAGSPWVRVARPVAVLRT 360
Db 301 LSAGIRCRPTTTRAVAICLAATLASRGVVAQPDAGVARAAAAGSPWVRVARPVAVLRT 360
QY 361 GPPRRPDSITQVGRPAVLFAPEQRCRRADQSCRQIHPPGGRHVQIVASARGTVE 420
Db 361 GPPRRPDSITQVGRPAVLFAPEQRCRRADQSCRQIHPPGGRHVQIVASARGTVE 420
QY 421 IGS 423
Db 421 IGS 423

RESULT 9
US-10-607-752-95
; Sequence 95, Application US/10607752

; Publication No. US20040072224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder
; FILE REFERENCE: 11000.1042c3
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US/10/607,752
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-10-607-752-95

Query Match 76.3%; Score 2184; DB 15; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.4e-148;
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLRDLAAR 60
Db 1 IYSTADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLRDLAAR 60
QY 61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPQORHARA 120
Db 61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAVGLGPQORHARA 120
QY 121 DGSISSALVAPPPRAASSAPASIGLPGSQHTSIHPRSSNGSPPTVHISQSMNAASSGTSR 180
Db 121 DGSISSALVAPPPRAASSAPASIGLPGSQHTSIHPRSSNGSPPTVHISQSMNAASSGTSR 180
QY 181 RSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEPAQORQKHRD 240
Db 181 RSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQGEPAQORQKHRD 240
QY 241 RDVPAQQRPAVHPAGPADRVGDPGRHRRARGOHQPRDGSQASRTVSGVPVSNV 300
Db 241 RDVPAQQRPAVHPAGPADRVGDPGRHRRARGOHQPRDGSQASRTVSGVPVSNV 300
QY 301 LSAGIRCRPTTTRAVAICLAATLASRGVVAQPDAGVARAAAAGSPWVRVARPVAVLRT 360
Db 301 LSAGIRCRPTTTRAVAICLAATLASRGVVAQPDAGVARAAAAGSPWVRVARPVAVLRT 360
QY 361 GPPRRPDSITQVGRPAVLFAPEQRCRRADQSCRQIHPPGGRHVQIVASARGTVE 420
Db 361 GPPRRPDSITQVGRPAVLFAPEQRCRRADQSCRQIHPPGGRHVQIVASARGTVE 420
QY 421 IGS 423
Db 421 IGS 423

RESULT 10
US-10-100-679-80
; Sequence 80, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c2
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US/10/100,679
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/450,072

```
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-100-679-80

Query Match          74.9%; Score 2145; DB 14; Length 582;
Best Local Similarity 67.4%; Pred. No. 1.3e-145;
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLRDLAAR 60
34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLRDLAAR 93
61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRRDVVGAGDAAAVGLGPQRHARA 120
94 HRSVGEVRGLGVFWA----- 108
121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
109 -GSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 167
181 RSSTLFRWQSPCMIPGSSAGLSRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKHLD 240
168 RSSTLFRWQSPCMIPGSSAGLSRESSQSASTCTDGNDSGA----- 207
241 RDVPAQORPAVHPAGPADRVGVDPGRRRARGQHOPRDSRQASRTVSGVPVESNV 300
208 -----GSDRQASRTVSGVPVESNV 226
301 LSAGIRCRTPPTTRAIVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
227 LSAGIRCRTPPTTRAIVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 286
361 GPPRRPSDT----- 370
287 GPPRRPSDTGSDQLGEPGAQQRQKHRRDRDVPAAQORPAVHPAGPADRVGVDPGRH 346
371 -----GSI TVGRPAVLFAPEQRCRRRADQSCROIHPGGRHVQIVASARGTV 419
347 RRARGQHOPRDSITQVGRPAVLFAPEQRCRRRADQSCROIHPGGRHVQIVASARGTV 406
420 EIGSTARLCGKDEAVALHYVAPVGEKQYIDRALNIGPYLPAEVPALV----- 469
407 EIGSTARLCGKDEAVALHYVAPVGEKQYIDRALNIGPYLPAEVPALVGSDDPERAGLR 466
470 -----GSIATGPPGTAWIVRQYPKLLR 493
467 VEVLGAQCRRRDVVGAGDAAAVGLGPQRHARADGSIATGPPGTAWIVRQYPKLLR 526
494 AKANWEDTWTFPSIEEKHPRGSVAGPVFRVNLGRAIPSRARAEEIHGSHHHHHH 549
527 AKANWEDTWTFPSIEEKHPRGSVAGPVFRVNLGRAIPSRARAEEIHGSHHHHHH 582

RESULT 11
US-10-607-752-80
; Sequence 80, Application US/10607752
; Publication No. US2004007224A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-06-26
```

```
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-607-752-80

Query Match          74.9%; Score 2145; DB 15; Length 582;
Best Local Similarity 67.4%; Pred. No. 1.3e-145;
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLRDLAAR 60
34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLRDLAAR 93
61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRRDVVGAGDAAAVGLGPQRHARA 120
94 HRSVGEVRGLGVFWA----- 108
121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
109 -GSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 167
181 RSSTLFRWQSPCMIPGSSAGLSRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKHLD 240
168 RSSTLFRWQSPCMIPGSSAGLSRESSQSASTCTDGNDSGA----- 207
241 RDVPAQORPAVHPAGPADRVGVDPGRRRARGQHOPRDSRQASRTVSGVPVESNV 300
208 -----GSDRQASRTVSGVPVESNV 226
301 LSAGIRCRTPPTTRAIVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 360
227 LSAGIRCRTPPTTRAIVAICLATLASRGVVAPOPAGDVAAAAAGSPWVRSVARPVAVLRT 286
361 GPPRRPSDT----- 370
287 GPPRRPSDTGSDQLGEPGAQQRQKHRRDRDVPAAQORPAVHPAGPADRVGVDPGRH 346
371 -----GSI TVGRPAVLFAPEQRCRRRADQSCROIHPGGRHVQIVASARGTV 419
347 RRARGQHOPRDSITQVGRPAVLFAPEQRCRRRADQSCROIHPGGRHVQIVASARGTV 406
420 EIGSTARLCGKDEAVALHYVAPVGEKQYIDRALNIGPYLPAEVPALV----- 469
407 EIGSTARLCGKDEAVALHYVAPVGEKQYIDRALNIGPYLPAEVPALVGSDDPERAGLR 466
470 -----GSIATGPPGTAWIVRQYPKLLR 493
467 VEVLGAQCRRRDVVGAGDAAAVGLGPQRHARADGSIATGPPGTAWIVRQYPKLLR 526
494 AKANWEDTWTFPSIEEKHPRGSVAGPVFRVNLGRAIPSRARAEEIHGSHHHHHH 549
527 AKANWEDTWTFPSIEEKHPRGSVAGPVFRVNLGRAIPSRARAEEIHGSHHHHHH 582

RESULT 12
US-10-100-679-94
; Sequence 94, Application US/10100679
; Publication No. US20030054013A1
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; CURRENT FILING DATE: 2003-06-26
```



```
/ FILE REFERENCE: 11000.1042c2
/ CURRENT APPLICATION NUMBER: US/10/100,679
/ PRIOR FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: PCT/NZ00/00121
/ PRIOR FILING DATE: 2000-07-10
/ PRIOR APPLICATION NUMBER: 09/450,072
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: 09/351,348
/ PRIOR FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 94
/ LENGTH: 372
/ TYPE: PRT
/ ORGANISM: Mycobacterium vaccae
US-10-100-679-94

Query Match      67.1%; Score 1919; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60
|||||
1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60
|||||

61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAAGVVGPGQRHARA 120
|||||
61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAAGVVGPGQRHARA 120
|||||

121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPTVHIQSMMNAASSGTSR 180
|||||
121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPTVHIQSMMNAASSGTSR 180
|||||

181 RSTLFRWQSPCMIPGASGLRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKGRD 240
|||||
181 RSTLFRWQSPCMIPGASGLRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKGRD 240
|||||

241 RRDVPAQQRPAVHPAGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
|||||
241 RRDVPAQQRPAVHPAGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
|||||

301 LSAGIRCRTPTTTRAVAIATLASRGVVAQOPAGDVARAAAAGSPWVRSVARPVAVLRT 360
|||||
301 LSAGIRCRTPTTTRAVAIATLASRGVVAQOPAGDVARAAAAGSPWVRSVARPVAVLRT 360
|||||

361 GPPRRPSDTGS 372
|||||
361 GPPRRPSDTGS 372
|||||

RESULT 13
US-10-607-752-94
/ Sequence 94, Application US/10607752
/ Publication No. US200400722441
/ GENERAL INFORMATION:
/ APPLICANT: Delcayre, Alain
/ TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
/ TITLE OF INVENTION: and Methods for Their Use
/ FILE REFERENCE: 11000.1042c3
/ CURRENT APPLICATION NUMBER: US/10/607,752
/ PRIOR FILING DATE: 2003-06-26
/ PRIOR APPLICATION NUMBER: 10/100,679
/ PRIOR FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: 09/450,072
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: 09/351,348
/ PRIOR FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 116
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 94
/ LENGTH: 372
/ TYPE: PRT
/ ORGANISM: Mycobacterium vaccae
```

```
US-10-607-752-94

Query Match      67.1%; Score 1919; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60
|||||
1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60
|||||

61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAAGVVGPGQRHARA 120
|||||
61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAAGVVGPGQRHARA 120
|||||

121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPTVHIQSMMNAASSGTSR 180
|||||
121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPTVHIQSMMNAASSGTSR 180
|||||

181 RSTLFRWQSPCMIPGASGLRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKGRD 240
|||||
181 RSTLFRWQSPCMIPGASGLRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKGRD 240
|||||

241 RRDVPAQQRPAVHPAGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
|||||
241 RRDVPAQQRPAVHPAGPADRVGDPGRHRRARGQHOPRDSRQASRTVSGVPVSNV 300
|||||

301 LSAGIRCRTPTTTRAVAIATLASRGVVAQOPAGDVARAAAAGSPWVRSVARPVAVLRT 360
|||||
301 LSAGIRCRTPTTTRAVAIATLASRGVVAQOPAGDVARAAAAGSPWVRSVARPVAVLRT 360
|||||

361 GPPRRPSDTGS 372
|||||
361 GPPRRPSDTGS 372
|||||

RESULT 14
US-10-100-679-79
/ Sequence 79, Application US/10100679
/ Publication No. US20030054013A1
/ GENERAL INFORMATION:
/ APPLICANT: Delcayre, Alain
/ TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
/ TITLE OF INVENTION: and Methods for Their Use
/ FILE REFERENCE: 11000.1042c2
/ CURRENT APPLICATION NUMBER: US/10/100,679
/ CURRENT FILING DATE: 2002-03-14
/ PRIOR APPLICATION NUMBER: PCT/NZ00/00121
/ PRIOR FILING DATE: 2000-07-10
/ PRIOR APPLICATION NUMBER: 09/450,072
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: 09/351,348
/ PRIOR FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 79
/ LENGTH: 582
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Made in a lab
US-10-100-679-79

Query Match      66.6%; Score 1906; DB 14; Length 582;
Best Local Similarity 57.1%; Pred. No. 2e-128;
Matches 399; Conservative 0; Mismatches 0; Indels 300; Gaps 2;

1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 60
|||||
34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLGFLDLAAR 93
|||||

61 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAAGVVGPGQRHARA 120
|||||
94 HRSVGEVRLGLVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAAAAGVVGPGQRHARA 153
|||||
```

```
Qy 121 ----- 120
Db 154 DGSQASRTVSGVPVSNVLSAGIRCTPTTTRAVAICLATLASRGVVAPQAGDVARAA 213
Qy 121 ----- 120
Db 214 AAGSPWVRSVARPVAVLRTGPPRRPSDTGSDQLGEPGAQQRGKHRRDRDVPAAQORP 273
Qy 121 -----DGSISSALVASPPRAASAPASIGLPGSGQ 150
Db 274 AVHPAGPADRVGVDPCRHRRRARGHQPRDGSISSALVASPPRAASAPASIGLPGSGQ 333
Qy 151 HTSIHPRSSNGSPTVHIISQSNMAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSAS 210
Db 334 HTSIHPRSSNGSPTVHIISQSNMAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSAS 393
211 TCTDNDGAGSDQLGEPGAQQRGKHRRDRDVPAAQORPAVHPAGPADRVGVDPCR 270
394 TCTDNDGSA----- 403
Qy 271 RRARGQHPRDGSQASRTVSGVPVSNVLSAGIRCTPTTTRAVAICLATLASRGVVAP 330
Db 404 ----- 403
Qy 331 QPAGDVARAAAGSPWVRSVARPVAVLRTGPPRRPSDTGSIITQVGRPAVLFAPEQR 390
Db 404 -----GSITQVGRPAVLFAPEQR 423
Qy 391 RRADQSCROIHPGGGRHVQIVASARGTVEIGSTARLCGKDEAAALHYVAPVGEKQDYI 450
Db 424 RRADQSCROIHPGGGRHVQIVASARGTVEIGSTARLCGKDEAAALHYVAPVGEKQDYI 483
Qy 451 DRALRNIGPYLPAEVPALVGSIAATGVPVGTAWIVRQYPKLLRAKANWEDTWTTPPSIEEK 510
Db 484 DRALRNIGPYLPAEVPALVGSIAATGVPVGTAWIVRQYPKLLRAKANWEDTWTTPPSIEEK 543
Qy 511 HPRGSGVAGPVFRVNLGRAIPSRARAABIIHGSHHHHH 549
Db 544 HPRGSGVAGPVFRVNLGRAIPSRARAABIIHGSHHHHH 582

RESULT 15
US-10-607-752-79
Sequence 79, Application US/10607752
Publication No. US2004007224A1
GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c3
; CURRENT APPLICATION NUMBER: US/10/607,752
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10/100,679
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/450,072
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/351,348
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-10-607-752-79
```

Query Match 66.6%; Score 1906; DB 15; Length 582;
Best Local Similarity 57.1%; Pred. No. 2e-128;
Matches 399; Conservative 0; Mismatches 0; Indels 300; Gaps 2;

```
Qy 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIIGEOVLGPGLRDLAAR 60
Db 34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIIGEOVLGPGLRDLAAR 93
Qy 61 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRRDVGAGDAAAAGVVLGPQRHARA 120
Db 94 HRSVGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRRDVGAGDAAAAGVVLGPQRHARA 153
Qy 121 ----- 120
Db 154 DGSQASRTVSGVPVSNVLSAGIRCTPTTTRAVAICLATLASRGVVAPQAGDVARAA 213
Qy 121 ----- 120
Db 214 AAGSPWVRSVARPVAVLRTGPPRRPSDTGSDQLGEPGAQQRGKHRRDRDVPAAQORP 273
Qy 121 -----DGSISSALVASPPRAASAPASIGLPGSGQ 150
Db 274 AVHPAGPADRVGVDPCRHRRRARGHQPRDGSISSALVASPPRAASAPASIGLPGSGQ 333
Qy 151 HTSIHPRSSNGSPTVHIISQSNMAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSAS 210
Db 334 HTSIHPRSSNGSPTVHIISQSNMAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSAS 393
Qy 211 TCTDNDGAGSDQLGEPGAQQRGKHRRDRDVPAAQORPAVHPAGPADRVGVDPCR 270
Db 394 TCTDNDGSA----- 403
Qy 271 RRARGQHPRDGSQASRTVSGVPVSNVLSAGIRCTPTTTRAVAICLATLASRGVVAP 330
Db 404 ----- 403
Qy 331 QPAGDVARAAAGSPWVRSVARPVAVLRTGPPRRPSDTGSIITQVGRPAVLFAPEQR 390
Db 404 -----GSITQVGRPAVLFAPEQR 423
Qy 391 RRADQSCROIHPGGGRHVQIVASARGTVEIGSTARLCGKDEAAALHYVAPVGEKQDYI 450
Db 424 RRADQSCROIHPGGGRHVQIVASARGTVEIGSTARLCGKDEAAALHYVAPVGEKQDYI 483
Qy 451 DRALRNIGPYLPAEVPALVGSIAATGVPVGTAWIVRQYPKLLRAKANWEDTWTTPPSIEEK 510
Db 484 DRALRNIGPYLPAEVPALVGSIAATGVPVGTAWIVRQYPKLLRAKANWEDTWTTPPSIEEK 543
Qy 511 HPRGSGVAGPVFRVNLGRAIPSRARAABIIHGSHHHHH 549
Db 544 HPRGSGVAGPVFRVNLGRAIPSRARAABIIHGSHHHHH 582
```

Search completed: September 16, 2005, 20:48:59
Job time : 173 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:44:49 ; Search time 43 Seconds
(without alignments)
1228.442 Million cell updates/sec

Title: US-10-607-752-116

Perfect score: 2862

Sequence: 1 IYSTFADRAYPGGLTSGHP.....IPSRARAARAEIHGSHHHH 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	273	9.5	451	2 T35390	probable aminotran
2	182	6.4	1442	2 T42607	transcription acti
3	172	6.0	1446	1 A45344	immediate-early pr
4	169	5.9	775	1 EDBE11	immediate-early pr
5	166	5.8	686	2 A38235	microtubule-associ
6	166	5.8	1733	1 B45344	probable nuclear a
7	163.5	5.7	2274	2 T30258	adenomatous polypo
8	157.5	5.5	1106	2 J00405	hypothetical 119.5
9	156.5	5.5	1958	2 B40505	hypothetical prote
10	156	5.5	2796	2 JC4743	fatty-acid synthas
11	151	5.3	660	1 Q0BE3	BHLF1 protein - hu
12	150	5.2	1952	2 T48814	hypothetical prote
13	148.5	5.2	744	2 T35192	probable ABC trans
14	147.5	5.2	426	2 B83611	4-aminobutyrate am
15	147	5.1	1298	1 EDBE75	immediate-early pr
16	147	5.1	13288	2 T03099	mucin, submaxillar
17	145.5	5.1	1334	2 T50568	probable multi-dom
18	144	5.0	1217	2 T00270	hypothetical prote
19	144	5.0	1329	2 T29074	hypothetical prote
20	142	5.0	1616	2 T17884	S-layer protein -
21	141.5	4.9	733	2 A45301	microtubule-associ
22	141.5	4.9	2082	2 T37056	probable multi-dom
23	140.5	4.9	924	2 T27923	gene LF3 protein -
24	140	4.9	825	1 EDBE4D	immediate-early pr
25	139.5	4.9	427	2 AF0839	4-aminobutyrate tr
26	139.5	4.9	1460	1 EDBE1F	immediate-early tr
27	139	4.9	1122	2 T14180	exit protein - Myc
28	138	4.8	1487	1 EDBE11	immediate-early pr
29	137.5	4.8	862	2 T46289	hypothetical prote

30 137.5 4.8 1496 1 CGHU2V collagen alpha 2(V
31 136.5 4.8 676 1 EDBE23 immediate-early pr
32 136.5 4.8 1487 1 EDBE6 155K transcription
33 136 4.8 467 2 T25848 hypothetrical prote
34 136 4.8 1607 2 T02837 long chain fatty a
35 135.5 4.7 538 2 S57459 hook-containing pr
36 135.5 4.7 888 2 S28791 collagen alpha 1(X
37 134.5 4.7 2240 2 T37057 probable multi-dom
38 134 4.7 1791 2 T02345 hypothetrical prote
39 133 4.6 1093 2 T38533 AF17 protein - hum
40 133 4.6 1678 2 T35547 hypothetrical prote
41 132.5 4.6 444 2 G90446 aminotransferase I
42 132.5 4.6 3869 2 A48205 AII-1 protein +GTE
43 132 4.6 527 2 A75399 hypothetrical prote
44 132 4.6 2142 2 B35098 MHC class III hist
45 131 4.6 317 2 S55316 mucin (clone PGM-2

ALIGNMENTS

RESULT 1

T35390

probable aminotransferase - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T35390

R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A;Reference number: Z21576

A;Accession: T35390

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-451 <MUR>

A;Cross-references: UNIPROT:Q9XA10; EMBL:AL079348; PIDN:CAB45489.1; GSPDB:GN00070; SCOE

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOE:SC66T3.33

C;Superfamily: ornithine-oxo-acid aminotransferase

Query Match 9.5%; Score 273; DB 2; Length 451;

Best Local Similarity 69.3%; Pred. No. 1.8e-09;

Matches 52; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 IYSTFADRAYPGGLTSGHPLACAVATINAMEDEGMVANAARIGQVLPGLRDLAAR 60

Db 298 IAATFAERPYPGGLTSGHPLACAAVATINVMAGVGVEHAARLGAEVVEPALRELAER 357

Qy 61 HRSVGEVRGIGVFWA 75

Db 358 HPSVGEVRGIGVFWA 372

RESULT 2

T42607

transcription activator - equine herpesvirus 4 (strain NS80567)

C;Species: equine herpesvirus 4

A;Variety: strain NS80567

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C;Accession: T42607; T42622

R;Telford, E.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.

J. Gen. Virol. 79, 1197-1203, 1998

A;Title: The DNA sequence of equine herpesvirus-4.

A;Reference number: Z22173; MUID:98264497; PMID:9603335

A;Accession: T42607

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-1442 <TEL>

A;Cross-references: UNIPROT:O42066; EMBL:AF030027; NID:G2605950; PIDN:AAC59599.1; PID:G2

A;Experimental source: strain NS80567

A;Accession: T42622

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-1442 <TE2>
A;Cross-references: EMBL:AF0300027; NID:g2605950; PIDN:AA059599.1; PID:g2606027
A;Experimental source: strain NS80567
C;Genetics:
A;Gene: 64
C;Superfamily: herpesvirus immediate-early protein IE175

Query Match 6.4%; Score 182; DB 2; Length 1442;
Best Local Similarity 21.4%; Pred. No. 0.0021;
Matches 136; Conservative 47; Mismatches 170; Indels 282; Gaps 28;

QY 5 PADRAYP-----GGLTYSCHPLATACAVATINAMEDGMVANAARICEQ----- 48
DB 542 YADWAYPRDDAGRODSHSAAGVTASYPAQAQ-----ASQPDPPATSAKRVETRYV 594
QY 49 -----VLGPGLR---DLAARHSVGEV-----RGLGVFWAGSDP 79
DB 595 CAALGPRTKTAAGGTRTPKPTAFRLRLRELGDCVCLACQAVFEALLRLRGASAVPGLDP 654
QY 80 ER-----AGLREVLGAQC---RRRDVVG-----AGDAAVGVLPQROH- 116
DB 655 SEIPSPACPPALCSNPAGLET-----AACALYELRDILVERARLLGDSDPHRLGPDRL 710
QY 117 -----RARADG-SISSALVASPPRAASSAPASIGLGPSCQHT 152
DB 711 AVRAVLVARTVAPLVYNAEGARARASAMTITQAVFSIFSLAGMLGEAVGL----- 763
QY 153 SIHPRSSNGPTV--HISQSMNAASGTSRRSSTLFEWQS---PCMIPGS-----ASSGL 202
DB 764 -LAPPRSQSSSVGDDVGGQQSSLSSEGSQTSRIPALWPTVPGLVVPATSHSQSSPQ 822
QY 203 RESQSASTCTDGNDSA---GSDLGEPGAQO----- 232
DB 823 HQSSGGPTTSRATQTQAPRSGQKARFPFAASAILQOEMPVSSQGGGPAPYASPNDRP 882
QY 233 ---RORGKRRDRDVPAAQPAVHPAGPGPADRVGDPGRHRRAGQHQPRDGSQDRQASR 289
DB 883 VNGPRKSKKRRSEPLE--PA---AGELPGSGGYDVPAPVSPAPKRVGT--QAPR 935
QY 290 TVSGVPVSVNLASGIR-----CRPTTTRAVAICLATLASRGVAPQAPAGDVARAAAAG 343
DB 936 ALGMPMPGEPHRRGGFRVPHGDCHTP-----PPGDSARAAYC- 973
QY 344 SPWPVRSVAPVAVLRITGPPRRPSDTGSIQVGRPAVLPAPEQRCRRADQSCRQIHP 403
DB 974 ---PPELVAELI-----DHPLPPEAWRPALTTFDQ----- 1000
QY 404 GGRHRVQIVASAGTVEIGSIARLCGKDEAVALHYVAVGEXQDYIDRALRNIGPYLPA 463
DB 1001 -----ALATIAACN-----GP--PA 1014
QY 464 EVPALVGSIAATGPVGTAMIVROYPKLLRAKANW 498
DB 1015 REGARFGELAASGP-----LRRRAAW 1035

RESULT 3
A45344
immediate-early protein - suid herpesvirus 1 (strain Kaplan)
C;Species: suid herpesvirus 1
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A45344
R;Vicek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzler, M.
Virology 179, 365-377, 1990
A;Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented or
A;Reference number: A45344; MUID:91021039; PMID:2171211
A;Accession: A45344
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-1446 <VLC>
A;Cross-references: UNIPROT:P33479; GB:M34651; NID:g334070; PIDN:AAA47470.1; PID:g334071
C;Superfamily: herpesvirus immediate-early protein IE175
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 6.0%; Score 172; DB 1; Length 1446;
Best Local Similarity 21.3%; Pred. No. 0.0085;
Matches 154; Conservative 54; Mismatches 224; Indels 290; Gaps 31;

QY 27 VATINAMEDGMVANAARICEQVLGPGLDLAARHR-SVGEVRLGLGVFWAGSDPERAGLR 85
DB 19 LAAAAAEEEGIAS-----GPDGSGQSRRRSGSGEDLLFGPGGLFSD-DAEAE 67
QY 86 VEVLGAQCRRRDVVGAGDAAVGVLP-----QOQHRARADGSI-----S 125
DB 68 AAVL-----AAAAGATFPPRPPSAQOQOQPRRSGEIVLDDDEDEDEFG 113
QY 126 SALVASPPRAASAPASIGLSPSGOHTSIHPRSSNGS---PTVHISQSMNAASGTSRR 181
DB 114 SPAAGSPGGA-----LHQSSEHGHVLGPRSRAGSGRPPTPAALAAAEAGAPGPGQR 166
QY 182 SSTLFRWQSPCMTPGSASSGLRESSQSASTCTDGNDSGAGSDOLGEPGAQQRQGHKRR 241
DB 167 SSP-----SAASPASSSGSPGSAAPRRWSPARGDPVGEPPGAARPTPAPPA 214
QY 242 RD-----VPAQORPAVHPAGP-----GPADRVGVDPQGRH-----R 271
DB 215 QPAAVAAAPARRGPA-SPASPAAGPVSAFGGGAAPSAGGDRGHHHQHREPLLDEPAAAR 273
QY 272 R-----ARG-----QHQPR-- 280
DB 274 RLDPRPLGARSPVSNPNNSNSTTTTAVETVARGPEKDEGLGLAGDGCAPPQPRRR 333
QY 281 -----DGSD-----RQASRTVSGVPVSVNLVS 302
DB 334 RAGEALRRGRGFSSSSSGSDLSLSPARSPAPRAAAAAARRSSSSSSSSSSSSSS 393
QY 303 A-----GIRCTPTTTRAVAICLATLASRG-----VVAPQPADGVARAAAAGSP 345
DB 394 SSSSEGEDEGVPCGAFLARA-----GPPSPAPAPAAAPRPSASSASSAAASP 442
QY 346 WPVRSVARP-----VAVLTGTPPPRPSDTGSIQVGRPAVLPAPEQRCRRRA- 393
DB 443 APAPEAPRPRRKRRTNNHLSLMADGPP---PTDGPLLTPLGEPWPGSDPPADGVRYG 499
QY 394 -----DQSCRQIHPGGRHVQIVASARGTV-----BIGSIARLCGKDEAVALH 438
DB 500 GAGDSREGLWEDDVQO-----AAARY-----RAAGVPVPIPEWGSRK---OHEALVRLI 549
QY 439 YVAPVGEKQDYD-----RALRNIGPYLPAEV-----PALVGSIAAT 475
DB 550 YSGAAGEAMSWLQNPQMOPDQRFNQFCQRRVHAPHGHGSFITGVTPLPHIGDAMAAQ 609
QY 476 GPVPGTAMIVROYPKLLRAKANWEDTWTTPSIEEKHPRGVSAGVPFRVNLGRAIPSRAA 535
DB 610 DPL-----WALPHAVSAAVMSRRYDRTKTFTILOSURRAYADWAYP-----GRAADPRAG 659
QY 536 RA 537
DB 660 EA 661

RESULT 4
EDBE11
immediate-early protein IE110 - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A29152
R;Perry, L.J.; Rixon, F.J.; Everett, R.D.; Frame, M.C.; McGeoch, D.J.
J. Gen. Virol. 67, 2365-2380, 1986
A;Title: Characterization of the IE110 gene of herpes simplex virus type 1.
A;Reference number: A29152; MUID:87059760; PMID:3023529
A;Accession: A29152
A;Molecule type: DNA
A;Residues: 1-775 <P>
A;Cross-references: UNIPROT:P08393; GB:X04614; NID:g59832; PIDN:CAA28285.1; PID:g59833
C;Genetics:

A: Introns: 19/3; 242/1
 C: Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
 C: Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F: 112-162/Domain: RING finger homology <RNG>
 F: 116-156/Region: zinc finger C3HC4 motif

Query Match 5.9%; Score 169; DB 1; Length 775;
 Best Local Similarity 23.4%; Pred. No. 0.0066;
 Matches 118; Conservative 38; Mismatches 164; Indels 184; Gaps 27;

QY 111 GPQHRARADGSISSALVASPPRAASAPASIGLG-----PSGQHTSI-----HP 156
 DB 307 GGSQSRAAA-----PRGASGPGGVGVGVVPAEAGRPGRGTGPIVNRPA 354
 QY 157 RSSNGSPVTHISQS-----MNAASGTSRSSTLFRWQSPCM 193
 DB 355 LANNEDPIV-LSDEPPASPHRPPAAMPGPSAPRPGPPASAAAGPAPRAAV-----APCV 409
 QY 194 -----IPGSASSGLRESSQSASTCTDGNDSGAGSDQLG 226
 DB 410 RAPPFGPRAPAPGAEPAPADARRVPQSHSSLAQAANQESLCCRATVARGSG--G 466
 QY 227 EPGAQORQKRRDRDVPQAPVAPVAPGADRVGDCRRHRRARGQHPQDGGSDRQ 286
 DB 467 GPGVE-----CGHGPSRGA-APSGAAPLPSAASVEQEAARVP-RKRRSGQENPQSTRP 520
 QY 287 -----ASRTVSGVPVSNVLSAGIRCR-----TPTRVAICLATLASRGVVAPOAGDV 336
 DB 521 PLAPAGAKRATHPPSDS-----GPGRGGGGTGTLTSSAASASSSSASS--SATPPAGAA 576
 QY 337 ARAAAGSPWVRVAREPAVL-----RTGPPRRPSTGTSITVQGRPAVLFP 385
 DB 577 SSAAGAASSASASGGAGVAGLGRQETSLGPRASGPRGP-----618
 QY 386 EQRERRADQSCROIHPGGGRHVQIVASAGTVEIGSIAR-----LCKDKEAVALHYV-- 440
 DB 619 -RKCAKT-----RH-----AETSGAVPAGGLTYLPISGVSSVVALSPYVNK 660
 QY 441 APVEKQDYIDRALRNIGPYLPAEVPALV-----GSIAA--TGPVGTAWIVR-----486
 DB 661 TITGDCPLDMETGNIGAYV-----VLVDQTGNMNLRAAVPG--WSRRTLLPETAGN 713
 QY 487 -----QYPKLLRAKANWEDTTFP 505
 DB 714 HVMPPEYP--TAPASEWNSLWMP 735

RESULT 5
 A38235
 A: Title: microtubule-associated protein, 110K tau - rat
 C: Species: Rattus norvegicus (Norway rat)
 C: Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C: Accession: A38235
 R: Goedert, M.; Spillantini, M.G.; Crowther, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 1983-1987, 1992
 A: Title: Cloning of a big tau microtubule-associated protein characteristic of the perip
 A: Reference number: A38235; MUID: 92179305; PMID: 1542696
 A: Accession: A38235
 A: Molecule type: mRNA
 A: Residues: 1-686 <GOE>
 A: Cross-references: UNIPROT: P19332; GB: M84156; NID: g207157; PIDN: AAA42204.1; PID: g207158
 A: Note: sequence extracted from NCBI backbone (NCBI: 87358, NCBI: 87359)
 C: Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C: Keywords: alternative splicing; microtubule binding; tandem repeat
 F: 497-527/Domain: MAP2/tau repeat homology <MT1>
 F: 528-558/Domain: MAP2/tau repeat homology <MT2>
 F: 559-589/Domain: MAP2/tau repeat homology <MT3>
 F: 590-621/Domain: MAP2/tau repeat homology <MT4>

Query Match 5.8%; Score 166; DB 2; Length 686;
 Best Local Similarity 22.8%; Pred. No. 0.0088;
 Matches 132; Conservative 69; Mismatches 189; Indels 188; Gaps 33;

QY 36 EGMVANAARICEQVLGFLRLDLAARH-----RSVGEVRGLGVF-W 74
 DB 88 EGTITABEAGIDT---PNMEDQAAGHTVQBPQKVEIFSQSLVTPGRREGQAPDSGISDW 144
 QY 75 -----AGSDPERAGLRV---EVLGAQCRDRDVVAGDAA--AVGVLGQR-----114
 DB 145 THQQVPSMSGAPLPPQGLREATHQPLGT--RPEDVERSHPASELLWQESPKQKAWKDRL 202
 QY 115 --QHRARADGSISSALVASPPRAASAPASI-----GLGPSGQHTSIHPRSSNGS-- 162
 DB 203 GSEBEVDIEDTMDSSOESPQSASLAPGTATPAQARSASGSGVGETTISIPGFPAGSIP 262
 QY 163 -PTVHISQSMNAASGTSRSTRSLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGA- 220
 DB 263 LPADFRSK-----VSAETQ-----ASPEPGTGPS--EEGHEAAPETFFHVEIKAS 307
 QY 221 -----GSDQIGEPQAQORQKQH--RDRRDV---PAQORPAVHPAG-PG-PADRVG 264
 DB 308 APKEQDLEGATVVGAPAEQKARGPSVGKGTKEASLLEPTDKOPA---AGLPGRPVSRV- 363
 QY 265 VDCGRHRRARGQHPQDGSQASRTVSGVPVSNVLSAGIRCTP-----TTTRA 314
 DB 364 --POLKARVAGVKDRGTGNDKKAAGADG-----KTGAKIATPRGAATPGQKGTNSA 413
 QY 315 VAICLATLAS-----RGVVAPOAPAGDVARAAAAGS-----PWPVRSVARPVAV 357
 DB 414 TRIPAKTTPSKTPPGSGEBPPKSGERSGYSSPGSGTTPGSRSTPSTLPTTPREPCKVAV 473
 QY 358 LRTGPPRRPSDGTSTVQGRPAVLPAPE--ORCRRADQSCROIHPGGGRHVQIVASAR 416
 DB 474 VRT--PPKSPASAKSLQT---APVMPDLKNVRSKIGSTENLKHQPGGK-VQII---N 524
 QY 417 GTVEIGSIARLCKDKEAV-----AALHYV-APV-----443
 DB 525 KLDLSNVQSKGSKONIKHVPGGSGVHIYKPVLSKVTSCGSLGNIHKKPGGQVEV 584
 QY 444 -GEKQDYIDRALRNIGPYLPAEVPALVPGVSAATGPPVPG 480
 DB 585 KSEKLDFKDR-----VQSKIGSLDNITHVPG 610

RESULT 6
 B45344
 A: Title: probable nuclear antigen - suid herpesvirus 1 (strain Kaplan)
 C: Species: suid herpesvirus 1
 C: Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C: Accession: B45344
 R: Vilecek, C.; Kozmik, Z.; Paces, V.; Schirm, S.; Schwyzer, M.
 Virology 179, 365-377, 1990
 A: Title: Pseudorabies virus immediate-early gene overlaps with an oppositely oriented op
 A: Reference number: A45344; MUID: 91021039; PMID: 2171211
 A: Accession: B45344
 A: Status: translation not shown
 A: Molecule type: DNA
 A: Residues: 1-1733 <UNIC>
 A: Cross-references: UNIPROT: P33485; GB: M34651; NID: g334070; PIDN: AAA47471.1; PID: g334072
 C: Superfamily: pseudorabies virus 1 nuclear antigen

Query Match 5.8%; Score 166; DB 1; Length 1733;
 Best Local Similarity 23.2%; Pred. No. 0.024;
 Matches 142; Conservative 45; Mismatches 218; Indels 208; Gaps 29;

QY 13 GLTYSGHPLATAC--AVATINAMEDEGMV---ANAAIRIGEQLV-----50
 DB 786 GVGVLPHPGGAAAERGAARFGDVRQGRVEGERAPEFGEDLLVHEGAGHLGRAVGEGR 845
 QY 51 --GFLRLDLAARHSVCEVRGLGVFWAGSDPERRAGLRVEVLGAQCRDRDVVAGDAAAVG 108
 DB 846 LGGPRRVGLAGRDAAEAIV--GRVL--GHGPERAPEV-VLGGG-----GGGQQRGSG 895
 QY 109 V-LGPQRQHRARADGS-----ISSALVASP-----PRAASSAPASIGLPGSG 149
 DB 896 VRSGPESGAALAPGPPVLFVAVAVAPAEGRAGEPLVLLAVPGAAGPRAALLAPLG 955

```
QY 150 QHTSIHPRSSNGSTVTHISQSNWAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSA 209
D 956 RWV-----RAGGGAGV-----AGGAGEAGL-----GAGAGL----- 982
QY 210 STCTDGNDSAGSDQLGEPGAQQRKHRRDRDVPQAQRPAVHP-----AGGPA 260
D 983 -----GAGAGLGAAGAGGAGGAGGARRRRRRRWDDEAGLJGPERGQAGRLGPGPR 1037
QY 261 DRVGVDGRRRRRARGQ-----HQRPRDGSRQASRTVSGVVPVESNV 300
D 1038 GGLG-EPGRGHVGRGEGRGVPGLAGAGPVHAVAQRHRRGAGDEGR-VRLGPLLGRA 1095
QY 301 LSAGIRCTPTTRAVAICLA-----TLASRGVVAPOPAGDVA-RAAAGSPWVRVA 352
D 1096 -GPDRAERAEQRGRHLLHLAGPGGRCGAGRG--OPERAGQQALEDAAAGQDAGVRLA 1152
QY 353 RPAVLRTGPPRRPSPDTSITQVRPAVLPAFQRCRRRADORSCRIHPGGGRHVQIV 412
D 1153 GHAAGLRGG-----EGGADAGBGLDR-----LPGAG----- 1180
QY 413 ASARGTVEIGSIARLCGKDEAAALHYVAVPVGEKQYIDRALRNIGPYLPAEVPALVGS 472
D 1181 --VRGAARVGHV-----GVGPAEALQDEGLLGA 1207
QY 473 AATGVPGTAWIVROYPKLLRAKANWEDTWTFFPSIEKHRRPRGSVAGVFRVNLGRAIPS 532
D 1208 VAAAHGHG-AHRVQGGPERVLGGHG-----VPDVRQ--RGHAAGDEGAVAVGRVDP 1257
QY 533 RAARAETHGSHH 545
D 1258 LAELVEALVGGHL 1270

RESULT 7
T30258
adenomatous polyposis coli protein 2 - mouse
N:Alternate names: APC2 protein
C:Species: Mus musculus (house mouse)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30258
R:van Es, J.H.; Kirkpatrick, C.; van de Wetering, M.; Molenaar, M.; Miles, A.; Kuipers,
Curr. Biol. 9, 105-108, 1999
A:Title: Identification of APC2, a homologue of the adenomatous polyposis coli tumour su
A:Reference number: 220796; MUID:99147086; PMID:10021369
C:Accession: T30258
Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-2274 <VAN>
A:Cross-references: UNIPROT:Q9ZLK7; EMBL:AJ130783; NID:94210431; PIDN:CAA10207.1; PID:94
C:Genetics:
A:Gene: APC2
A:Introns: 47/3; 78/1; 138/2; 174/3; 212/3; 238/3; 271/3; 396/1; 428/1; 474/3; 500/3; 53

Query Match 5.7%; Score 163.5; DB 2; Length 2274;
Best Local Similarity 24.1%; Pred. No. 0.045;
Matches 126; Conservative 56; Mismatches 191; Indels 149; Gaps 26;

QY 79 PERA-GLRVEVLG--AQCRRRDVV-GAGDAA---AVGVLGPQRQHRARADGSISSALVAS 131
D 1742 PEKAGTQKMAGESTMLRGRTVIYSAGPASRTQSGISGP-----CTT 1785
QY 132 PPRAASA---PASIGLGPQGH---TSIH-----PRSSNGSPVTHISQSM 171
D 1786 PKTGTGTTQPTVITVAPSPQQRSLRHPGKISLAALRHPPRSA--TPPARLAKTP 1843
QY 172 NAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQASTCTDGNDSAGSDQLGEPGAQ 231
D 1844 SSSSSQTSASQPLPR-RSPLATP-----TCGPLPGGSLVPKSPAR 1885
QY 232 QRQGRKHRRD---VPAQQRPAVHPAGPADRVGDPGRHRRARQCHOP-----RDGS 283
D 1886 ALLAKQHKTKSPVRIIPFMQRPARRV--PPPLARPSPEPGSRGAGAEFTFGAGSRGLG 1943
```

```
QY 284 DRQASTVTSVGV-----PVESNVLSAGIRCTRP 310
D 1944 VRMASARSSGSESSDRSGFRRLQTLFIKESPLGRLRRRSELSSADSTASTSQAAAPRGRP 2003
QY 311 TTTRAVAICLAUTLASRGVVAPOPAGDVARAAAGSPWVRVAAPVAVLTG--PPRRP- 367
D 2004 ALPAVFLCSCRDELKVSROP-----LAAQSRSPQAKPGLA-FLAPRRTSESPSRLPV 2056
QY 368 -SDTGSITQVRPAVLPAFQRCRRRADORSCRIHPGGGRHVQIVASARGTVEIGSIAR 426
D 2057 RASPGPEITVKRYASL--PHISVSRSDS-----AVSVPTTQANATR 2097
QY 427 LCGKDEAAALHYVAPVGE-----KQYIDRALRNIGP--YLPAEVPALVGSTAAATGPVP 479
D 2098 --GSDGEARPLPRVAPGTWTRIKDEDPHILRLSTLPATALPLRVSSPEDSPAGT-PQR 2154
QY 480 GTAWIVROYPKLLRAKANWEDTWTFFPSIEKHRRPRGSVAGPV 521
D 2155 KTSDAVVQTEDVATSKTN---SSTSPSLESRPDPQAPASGPV 2193

RESULT 8
JQ0405
hypothetical 119.5K protein (uvrA region) - Micrococcus luteus
N:Alternate names: ORF 1 protein
C:Species: Micrococcus luteus, Micrococcus lysodeikticus
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Feb-2000
C:Accession: JQ0405
R:Shiota, S.; Nakayama, H.
Mol. Gen. Genet. 217, 332-340, 1989
A:Title: Micrococcus luteus homolog of the Escherichia coli uvrA gene: identification of
A:Reference number: S04781; MUID:89364717; PMID:2549377
A:Accession: JQ0405
A:Molecule type: DNA
A:Residues: 1-1106 <SHI>
A:Cross-references: EMBL:X15867
A>Note: this reading frame extends between two stop codons and does not begin with a sta
A>Note: the gene encoding this protein overlaps uvrA gene
C:Superfamily: collagen alpha 1(i) chain; fibrillar collagen carboxyl-terminal homology;

Query Match 5.5%; Score 157.5; DB 2; Length 1106;
Best Local Similarity 24.5%; Pred. No. 0.048;
Matches 151; Conservative 37; Mismatches 220; Indels 209; Gaps 31;

QY 57 LAARHSRVEVRGLGVFWAGSDPERAGLRFVEVLGAQCRRRDVVGAGDAAV----- 107
D 423 LAARARRAGQGDCLLPGHVPEGPDGGAR-----RRPARQGLQGGGDVPQVPRAPLHH 477
QY 108 GVLG--PQRHARADGSISSALVASPPRA-----ASSAPASIGLGPSCQHTSIHPRSN 160
D 478 GURGRHLDAQARGD-----RVGRRPALRVVHAGDPVPGVPRGPPQPH---GPERAR 528
QY 161 GSPVTHISQSNWAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQASTCTDGNDSGA 220
D 529 GRP-VHRGRHPPAHARGH-----VLLGAADG-----PGAADRG 563
QY 221 GSDQLGEPG-----AQQRGKHRRDRDVA-----QORPAV 252
D 564 GAO--GDPGPAVGPAGRRPRVPQRAAGRHPLRRRGFAHPGHTDLRAGRRLRPRRAV 621
QY 253 H---PAGCPADR---VGVDPCRH---RRRQCHQPRDGSDR--QASR-----TVSGV 294
D 622 HRPAPAGQPPPHRDPPAPAGPQHPHRRRARRCHDRGGLDGRHRSRGRVRRRGALGL 681
QY 295 PVESNVLSAGIRCTPTTRAVAICLAUTLASRGVVAPOPAGDVARAAAGSPWVRVAAP 354
D 682 PGSGQGEHAVRRRLP-----LRPPLHRGAGAAARPCGEARADG-----PRRGEQF 728
QY 355 VAVLRTPGPPRRPSPDTSITQVRPAV-----LFAQRCCRRAADQSCRIHPG 404
D 729 EG--RLGPGPAR---GPHGRDGRVRLRVHADRQDFLQGGQPAQR--QARARPAVR 780
```

Query Match	5.5%; Score 156.5; DB 2; Length 1958;
Best Local Similarity	21.0%; Pred. No. 0.1;
Matches	126; Conservative 51; Mismatches 247; Indels 175; Gaps 21;
QY	13 GLTYSGHPLATACAVATINAMEDGMVANAARIGEQVLGPLRLDLAARHSRSGEV-RGLG 71
Db	996 GVGYLPHIP-GGAABERGARGPAAGDVROQGRVEGERRAPEFGEDLLVHBGAGHLGRAVG 1054
QY	72 VFWAGSDPERAGLRVEVLGAQCRRRDYYVGAGDAAAV-----GVLGFORQHRARAD 121
Db	1055 GEGRGCGPRRVLAGRDAEAAVGRGVLGHGPERAPEPVVLGGCGGGGGGHERGSGVRSG 1114
QY	122 GSTSSALVASSPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHTISQSNVAASSGTSRR 181
Db	1115 PESGAALAPGPPVPLFVVAVAVAPAEGR-----AGEPLVLLAVGAAGGFGRAALL 1165
QY	182 SSTLFRWQSPCMTIPGSASSGLRESSQASCTD-----GNDSGAGSDQIGEPGAOQRQKX 238
Db	1166 LAPLGRW----VRAGCGGAGVAGGAGBAGLGAAGLGAAGLGAAGGAGGPGGAGCGGAR 1221
QY	239 RRRDRVPAOQRPVAVHP-----AGGPGADRVGVDPGRHRRARGO----- 276
Db	1222 RRRRRRWDDEAGLLGPERGQAGRLGPGFGGLG-EPGPGHVGRGEEGRGVGPGGLAGA 1280
QY	277 -----HQPRDGS-----DRQASRTVSGVPVESNVLSAGIRCTP 310
Db	1281 GPVHAVAHQRHHGAGDEGDRVGRLLPLIGRAGPGDRVAEREQRG-----GHLLERAG----- 1330
QY	311 TTRAVAICLATLASRGVVA--POPAGDVA-RAAAGSGPWPVRSVARPVAVLRTGPPRR 366
Db	1331 -----GPEGRGAGRGQPERACQQALEDAAQGDAGVQLAGHAGLKG--EG 1378
QY	367 PSDTGSTVQGRPAVLPAPEQRCCRADQRSCKRIHPGGRGHVQIVASARGTVEIGSIAR 426
Db	1379 GADAGAEGLDGR-----LPGAG-----VGAARVGVH-- 1405
QY	427 LCGKDEAVAAHLHYVPAVGEQDYIDRALRNIGPYLPFAVEPALVGSTAATGPVGTAWIVR 486
Db	1406 -----GVGPAEALQDEGLLGAIVAAAHGG-ARRVR 1435

Query Match	5.5%;	Score 156;	DB 2;	Length 2796;
Best Local Similarity	22.3%;	Pred. No. 0.16;		
Matches 148;	Conservative 59;	Mismatches 216;	Indels 242;	Gaps 34

QY	1	IYSTFADRAYPGGLTYS--GHPLATACAVATINAMEDEGMVANAAIRIGBQVLGPGGLRLDAA	59
DB	204	IVAGWAEGA---GLDVALARELADAILIRKVDWVDEITRVHRAGARWILDLOGP--DILT	258
QY	60	RHRSGEVRGLGVFWAGSDPERAGLRVEVLGAQCRRDDVVGAGDAAAVGVLGPOQRHAR	119
DB	259	R-LTAPVIRGLGI---GIVPAR-----TRGGQ--ENLFTVGATPEV-----AR	295
QY	120	ADGSGISSALVASP-----PRAASSAPASI--GLGPSQHTSIHPRSSNG-----	161
DB	296	AWSSYAPTVVRLPDGRVKLSTKFTLRRSPILLAGMTPTVDAKIVAAAANGRHWAE	355
QY	162	-----SP---TVHISQNNAASSGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSASTCTD	214
DB	356	ARGSRKRSVTTASNKPWACSSRAAPTSIT--RCSS---IPTCEASGGRQAVGAEGPPVR	410
QY	215	GNDSGAGSDQLGPGGAQO---RORCKH-----RDRRDVP---AQORPAVHPAGP	257
DB	411	RRDRRG--DQRHPRPRGRADRTGRHRHQPRVQTRDHRADPLGDSHHRGNAHQAGD	469
QY	258	-----GPADRVGVDPGR-----HRRARGQHQ-----PRDG-----	282
DB	470	HARRGPCAPAGTTPGRISHILLATYSADRAPRQHHCVGVGGHLGTPKKCGCYLSPGGRSV	529
QY	283	-----SDRQ-----ASRTVSGVPVYES-----NVLSAG-----IRCR	308
DB	530	RLPIDADRRLVCTAAMATKESITTSVSKRMVLDTQGTQDWISAKGAGRMPPAESARCR	589
QY	309	TPPTR---AVAIC-----LATLASRGVVAPOPAGDVAR-----AAAAAGSPWPFVRSV	351
DB	590	HPDRHSASVRRGSTRWPTVTRRSRSVAVPRPPSPTCRRRRHDLPAVAAGATSNWPSGKA	649
QY	352	ARRVAVLRTGPPRRRSDTGSITQVGRPAVLFAPEQCRRRADQRSCH-----	399
DB	650	TRP-----PTPRWAARGWPTLAG-----PLADAAACRSFVATGFRDPP	690
QY	400	-----QIHPGG-----GRHVQIVASARGTV	419

Db 691 DAIRHCWPAGQSAALVALVARYPDAETVQLHPADVPFFVTLCKTKLPVNFVPAIDLIV 750
Qy 420 EIGSIARLCGKDEAVA-----ALHYVAPVKGQDYIDRALRNIIGYLPFAEVPALVGSIAA 474
Db 751 RAGGAATRCGRPTTPTATPMRCASFRAVRSR---ITRMDPEVGGELDAFEQAIDEVLG 807
Qy 475 TGPVP 479
Db 808 AGVEP 812

RESULT 11
QOBE3
BHLF1 protein - human herpesvirus 4 (strain B95-8)
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C:Accession: A03742
Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Biol. Med. 1, 21-45, 1983
A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
A:Reference number: A93065; MUID:85035713; PMID:6092825
A:Accession: A03742
A:Molecule type: DNA
A:Residues: 1-660 <BAN>
A:Cross-references: UNIPROT:P03181
R;Bar, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A:Reference number: A03794; MUID:84270667; PMID:6087149
A:Comments: annotation; protein coding region
C:Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52
C:Superfamily: human herpesvirus 4 BHLF1 protein

Query Match 5.3%; Score 151; DB 1; Length 660;
Best Local Similarity 27.4%; Pred. No. 0.069;
Matches 131; Conservative 25; Mismatches 188; Indels 134; Gaps 27;

Qy 100 GAGDAAAVGLGPOQH-RARADGSISSALVAPPPRAASAPASIGLPGSGQHTSIHPRS 158
Db 219 GPADPPAAALPPPERQFRLPQDLAAQRCPCAGPPPTRSGAAA-----QTHRRP-- 268
Qy 159 SNGSPVTHISQSMMAASGTSRSSTLFRWQSPCMIPG-----SASSGLRESSQSA--ST 211
Db 269 -PGCP-----RSARNPCPTWRRRSGAQRHPP---PGAQRSFGTGGPAPAGAPGT 320
212 CTGNDGSA-----GSDQGEPAQO--RQRKHRRDRDVPAAQRPVAVHPAG 257
321 AAPGPGGAAVPSGATPHPERGSGPADPPAAARLPPERQFRLPQDLAAQRCPCAGP 377
Qy 258 GPADRVG-----DPGHRHRRARGQHPDQSDRQASTVSGVPVESNLVAGIRCT 309
Db 378 -PPTRSGAAQRTHRRPPGCFRSARNPCPTWRRRSGAQRHPP-----GAGQRP 430
Qy 310 PTTTAVAIATLASRGVAPQAGDVARAAAAGSPWVR--SVARFVAVLRGP---PP 364
Db 431 PTGGERPA---APGAGTTPAPGCGGAAPVSGA--TPHPERGSGPADPPAAARLPPERQEP 486
Qy 365 RRPDSITQ--VGRPAVL--APEQRCRRAD--QRSCQIHFGGGRHVQIVASA-RGT 418
Db 487 RLPQDLAAQRCPCAGPPPTRSGAAQRTHRRPPGCPESAR--NFGCPRTWRRRSGAQRH 544
Qy 419 VETGSIARLCGKDEAVAALHYVAPVKGQDYIDRALRNIIGYLPFAEVPALVGSIAATGPV 478
Db 545 PPPGAGQRP 576
Qy 479 PGTAWIVRQYPKLLRAKANWEDTTFPSIEEKHPRGSGVAGPVFVNLGRAIPSRAR 536
Db 577 GGAA-----VPSGATPHRGS-----GPADPPAAR 603

RESULT 12

T48814

hypothetical protein 1586.220 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C:Accession: T48814

R;Schulte, U.; Algn. V.; Hobeisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000

A:Reference number: 224541

A:Accession: T48814

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1952 <SCH>

A:Cross-references: UNIPROT:Q9P6T1; EMBL:AL353822; GSPDB:GN00112; NCSP:1586.220

A:Experimental source: cosmid contig 1586; strain 74

C:Genetics:

A:Gene: NCSP:1586.220

A:Map position: 2

A:Introns: 281/3

Query Match 5.2%; Score 150; DB 2; Length 1952;

Best Local Similarity 22.0%; Pred. No. 0.25;

Matches 135; Conservative 56; Mismatches 246; Indels 176; Gaps 27;

Qy 11 PGGLTYSGHPLATACAVATINAMEDGVMANARIGEQLVGLGLRDLAARHSVGEVRGL 70

Db 1292 PRAAPISGHPIAP-----STVNN-----TNAAM-----GARVPA----- 1321

Qy 71 GVFWAGSDPERAGLRVEVLGAQCRRRDVVAGDAAAVGLGPOQRHARADGSISSALVA 130

Db 1322 -----AVGPQ-----IGVHSGAAGVTPVPSRPPVTHGVVTAAPT 1359

Qy 131 SPRAASSAPASIGLPGSQHTSIHPRSSNGSPTVHISQSMMAASGTSRRS-----STLF 186

Db 1360 TP---RSNLAAVFPAGSMAQOT--HSGAPAGSGNASISRAPPTAAPTAPTSPVPSSTV 1414

Qy 187 RWQS--PCMIPGSASSGLRESSQASTCTGDNDSGAGSDQLGEPG-----AQQRK 235

Db 1415 RPSYVTPGPGGLTAPPTASSGASAGYARPANASTMPATISQAAMTSVAVPOSVPSPRS 1474

Qy 236 GKHRDRDVA-----QQRPAVHPAGPGPADRVGDVDPGRHRRARGQHQPDRGSDRQASRT 290

Db 1475 SLTTGQMGVPAIAAAASTSRPASGVNYP--PASSLA--PSTHK-----SMPSAVPT 1520

Qy 291 VSGVPVESNLVAGI-----RCRTPTTAVAIATLASRGVAVPQAGDVA 337

Db 1521 TASGAVSSTVSSLAATPLPSAPRYGPSNNATPTTATAPRAPLPAASSVAPVTTGQPS 1580

Qy 338 RAAAAGSPWVRSA-----RPVAVLRTPPPRPSPDTSITQV-----GRPAVLFP 385

Db 1581 FSAPASVPTPTTSAASQGAQLSQPV-----GPAPAISSSIGATPAASTPSSAPALAPV 1635

Qy 386 EORCRRRQRCR-QIHFGGGRH--VQIVAS--ARGTVE--IGSIAR-LCGKDEAVAAL 437

Db 1636 TYPVPOQASAAAARLFPVTPAPAAHTIAQSVAFVPTQSPVQSVQVACHVTSQAATTA 1695

Qy 438 HVVA-----PVGEK-----QDYIDRALRNIIGYLPFAEVPALVG 470

Db 1696 HPVAGSVPRVNSNPTSAPAAVAVGTAQVASAPVTQAPAPHRALSSVLSLQSVPHAAQ 1755

Qy 471 SIAATGVPFGTAWIVRQYPKLLRAKANWEDTTFPSIEEKHPRGSGV-----GPVF 522

Db 1756 QAAHQTFHSASRPVQSVFQ-----SVQATQAVPRPSTSLTPTAQGPVS 1803

Qy 523 RVNLGRAIPSR 535

Db 1804 PAVSGSGVPAPSA 1816

RESULT 13

T35192

probable ABC transporter - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C:Accession: T35192

R;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1998

A;Reference number: 221571
A;Accession: T35192
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-744 <SE>
A;Cross-references: UNIPROT:O69995; EMBL:AL02374; PIN:CAA18516.1; GSPDB:GN00070; SCORE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SC05B8.08

Query Match 5.2%; Score 148.5; DB 2; Length 744;
Best Local Similarity 24.2%; Pred. No. 0.11;
Matches 130; Conservative 53; Mismatches 215; Indels 139; Gaps 27;

QY 18 GHPLATA-----CAVATTINAMEDEGMVANAARIGEOVLGPGRLDLAARHRSVGEVRL 70
DB 85 GHFARTVRGHLRMLCAAAGV-----PVRRADVEVLSVGLLGRDLRDLGSLRGMDRL 137
QY 71 GVFWA-GSDP-----ERAGLRVEVLGAQCRRRDVGAGDAAAVGVILGPQRQHRARADGS 123
DB 138 GLACALVPDPHTLVFDDPAG-----ALSAHDAR--GLHGALRAHAQAQGTV 181
QY 124 ISSALVASPPRASSAPASIGL-----GPSGQHTSIHPRSSNGSPVTHISQMN 173
DB 182 LFS--TADPKAARSADHVVTLEGRVYVADQEAFAEFSTRRLRPVAVRSPHAARLAALVT 239
QY 174 ASSGTSRSTLRFWQSPCMIPGSASSGLRESQSASTCTDGNDSGAG-----SDQL 225
DB 240 KEAARARSVEVVR-----EGGNRLVYGSTCADIGEAFAFRHGILVHQLADEV 287
QY 226 GE--PGAQQRQGRKRRDRVPAQRPV-----HPAGPG---PADRVGVDPGRHRR 272
DB 288 GDMGPGAGEIPAAQQRERADGAPGTGTLNAGRPGPTPGVLLFSPATEGEPLDGR 347
QY 273 ARGQHOPRDG-----SDRQASRTVSGVPVVSNLVLSAGIRCTPTTTRVAICLAT 321
DB 348 GAG-HGDDGDPASVAVNRTPGPRQAPVAPVSGHGEA-----APSPAPAPGPSE 396
QY 322 LASRGVVAPOPAGDVARAA--AAGSPWVSVARVPVAVLTGPPRRPSTGSIQVGRP 379
DB 397 PAS-GPSAPAP-GPPAPAGSPAPAGFSPAPAGPSA---PAPGPSEPAGSPAPAG-P 450
QY 380 AVLFAPEQRCCRADQSCRIHPGGGRHVQIVASARGTVEIGSIARLCGKDEAVAAHY 439
DB 451 SALDAEPLR-----TPRPFALVPGSARTREATATLPPISVRS-----APSPLEPLRY 499
QY 440 V--APVGEKQDYIDRLRNTGYPVLPAPVPAVLSIAATGPVPGTAMIVROYPKLLRA 494
DB 500 ELRRVAVGRTGFTGAV---VLLVSAVAVV--LARVGHTP-----QPELLAA 542

RESULT 14
B83611
4-aminobutyrate aminotransferase PA0266 [imported] - Pseudomonas aeruginosa (strain PA01
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B83611
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: B82950; MUID:20437337; PMID:10984043
A;Accession: B83611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <STO>
A;Cross-references: UNIPROT:Q916M4; GB:AE004465; GB:AE004091; NID:g9946107; PIDN:AA0368
A;Experimental source: strain PA01
C;Genetics:
A;Gene: gabT; PA0266
C;Superfamily: ornithine-oxo-acid aminotransferase

Query Match 5.2%; Score 147.5; DB 2; Length 426;
Best Local Similarity 33.7%; Pred. No. 0.07;
Matches 34; Conservative 23; Mismatches 35; Indels 9; Gaps 3;

QY 7 DRAYPGGL--TYSGHPLATACAVATTINAMEDEGMVANAARIGEOVLGPGRLDLAARHRSV 64
DB 288 DATAPGGLGTAGSTAGSIACAAALAVLKVFEELKLSRQVGR-LKAGLREIQAKHKVI 346
QY 65 GEVRGLG-----VFWAGSDPERAGLRVEVLGAQCRRRDVV 99
DB 347 GDVRGLGSMVAIELFEGGDTKPAABELVSKIVVRAREKGLI 387

RESULT 15
EDBE75
Immediate-early protein IE175 - human herpesvirus 1
C;Species: human herpesvirus 1
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A23510
R;McGeoch, D.J.; Dolan, A.; Donald, S.; Brauer, D.H.K.
Nucleic Acids Res. 14, 1727-1745, 1986
A;Title: Complete DNA sequence of the short repeat region in the genome of herpes simple
A;Reference number: A23510; MUID:86148504; PMID:3005980
A;Accession: A23510
A;Molecule type: DNA
A;Residues: 1-1298 <MCG>
A;Cross-references: UNIPROT:P08392; GB:XL14112; GB:D00317; GB:D00374; GB:S40593; NID:g194
C;Comment: This protein acts at the transcriptional regulatory level and is required thr
C;Genetics:
A;Gene: IE3
A;Map position: short repeat region (IR-s)
C;Superfamily: herpesvirus immediate-early protein IE175
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 5.1%; Score 147; DB 1; Length 1298;
Best Local Similarity 22.2%; Pred. No. 0.25;
Matches 136; Conservative 56; Mismatches 205; Indels 216; Gaps 32;

QY 8 RAYPGGLTYSGHPLATACAVATTINAMEDEGMVANAARIGEOVLGPGRLDLAARHRSVGEV 67
DB 472 RAYAPLLARENAALTGAAGSPGAGA--DDEGVAAVAA-----AAPGERAVPAGYGAAGIL 524
QY 68 RGLGVFWA-----GSDPER-----AGLR-----VEVLGAQCRRRDVVGA--- 101
DB 525 AALGRLSAASPAGGDDDDAARHADDDAGRAAGRAVAVECLA-C--RGILEALAE 581
QY 102 ---GDAAAV-GVLGPQRQHRARADGSISSALVASPP-----GQHTSIH 155
DB 639 LMRLRGDLRVAGGSEAAVAVRAVSLVAGALPRDPRPLPSSAAAAADLLFDNQSLR 698
QY 156 PRSSNGSPVTHISQMNAAASGTSRSTLFRWQSPCMIPGSASSGLRESQSASTCTDG 215
DB 699 PLLAAASAPDADALAAASNAAPREGKRKSPGPAPPGGGGPPPKTKS----- 751
QY 216 NDSGAGSDQLGFBGAQORQGRKRRDRVPAQQRPAVHPAGPAGPADRVGVDPGRHRRARG 275
DB 752 ----GAD--APGSDA-----RAPLPAPAPPST--PPGPEPAP---AQAAPRAAAA 791
QY 276 QHQPRDGSQRQASRTVSGVPVVSNLVLSAGIRCTPTTTRVAICLATLSRGVVAPOPAGD 335
DB 792 QARPREVA-----VSRPAPGDPDLGGWR-RQP-----PGFSHT 824
QY 336 VAAAAAGSPWVSVARVPVAVLTGTPRRRPSDTGSIQVGRPAVLFAPE-----QRC 389
DB 825 AAPAAAA-----LEAYCSRAVAELTDHPLFPVP-----WRPALMFDPRALASTAARC 872
QY 390 R--RRADQRSC-----RQHPGGGRHVQIVASARGTVEIGSIARLCGKDEAVAAHYVA 441

Db 873 AGPAPAAACGGDDDDNPHPHGAAGRLFGPIRAS---GPLRRMAA-----WMR 920
QY 442 PVGEKQDYIDRALRNIGPYLPAEVPAIVGSIAATGPVPGTAWIVRO--YPKLLRAKAN-- 497
Db 921 QIEDPED-----VRVVVLYSPLFGEDIAGGGASGGP---PEWSAERGGLSCLIAALANRL 972
QY 498 -----WEDTWT 503
Db 973 CGPDTAAWAGNWT 985

Search completed: September 16, 2005, 20:55:54
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:36:13 ; Search time 179 Seconds
(without alignments)
1570.567 Million cell updates/sec

Title: US-10-607-752-116
Perfect score: 2862
Sequence: 1 IYSTFADRAYPGGLTYSCHP.....IPSRARAAEIHGSHHHH 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	284	9.9	451	2 Q82ER2	Q82er2 streptomyc
2	273	9.5	451	2 Q9XA10	Q9xa10 streptomyc
3	202.5	7.1	469	2 Q8FN12	Q8fn12 corynebacte
4	185.5	6.5	608	2 Q9Q5K9	Q9q5k9 herpesvirus
5	182	6.4	1442	2 Q42066	Q42066 equid herpe
6	182	6.4	2087	2 Q8MXL2	Q8mxl2 leishmania
7	180	6.3	438	2 Q8NMX2	Q8nmx2 corynebacte
8	180	6.3	456	2 Q842J4	Q842j4 corynebacte
9	180	6.3	456	2 Q6M323	Q6m323 corynebacte
10	179.5	6.3	1408	2 Q6X125	Q6x125 bovine herp
11	179	6.3	1422	2 Q82D83	Q82d83 streptomyc
12	176.5	6.2	1461	1 IE18_PRVIF	P1675 pseudorabie
13	174	6.1	3889	2 Q6SS58	Q6sse8 chlamydomon
14	173.5	6.1	1783	1 RAA3_CHLRE	Q9fec4 chlamydomon
15	172	6.0	1446	1 IE18_PRVKA	P33479 pseudorabie
16	170	5.9	813	2 Q8GFF3	Q8gff3 streptomyc
17	169	5.9	775	1 ICF0_HHV11	P08393 human herpe
18	169	5.9	990	2 Q9BLV0	Q9blv0 leishmania
19	168	5.9	581	2 Q6H509	Q6h509 oryza sativ
20	168	5.9	816	2 Q7QWN8	Q7qwn8 giardia lam
21	167.5	5.9	579	2 Q8GFF2	Q8gff2 streptomyc
22	166	5.8	1733	1 VNUA_PRVKA	P33485 pseudorabie
23	165.5	5.8	2658	2 Q9GRU9	Q9gru9 leishmania
24	164.5	5.7	1479	2 Q82FF7	Q82ff7 streptomyc
25	164	5.7	865	2 Q62DN2	Q62dn2 burkholderi
26	163.5	5.7	2274	2 Q9Z1K7	Q9z1k7 mus musculu
27	162.5	5.7	1685	2 Q3UEW8	Q3uew8 homo sapien
28	162	5.7	382	2 Q8S0V8	Q8s0v8 oryza sativ
29	162	5.7	438	2 Q63JU4	Q63ju4 burkholderi
30	161.5	5.6	1187	2 Q8P8Z4	Q8p8z4 xanthomonas
31	161	5.6	1345	2 Q9L060	Q9l060 streptomyc

32	160.5	5.6	2303	2	Q95996	Q95996 homo sapien
33	158	5.5	1454	2	Q8JL63	Q8jl63 suid herpes
34	157	5.5	1841	2	Q63VY6	Q63vy6 burkholderi
35	156.5	5.5	1958	2	Q89340	Q89340 suid herpes
36	156	5.5	821	2	Q8VPM9	Q8vpm9 micrococcu
37	156	5.5	1463	2	Q9ADP6	Q9adp6 streptomyc
38	156	5.5	2796	2	Q48926	Q48926 mycobacteri
39	154	5.4	1684	2	Q91LK9	Q91lk9 white spot
40	153.5	5.4	595	2	Q6YX66	Q6yx66 oryza sativ
41	153.5	5.4	1240	2	Q9DWH8	Q9dwh8 rat cytomeg
42	153	5.3	1014	2	Q8YOK3	Q8yok3 raietonia s
43	153	5.3	1111	2	Q9L0P1	Q9l0p1 streptomyc
44	153	5.3	1937	2	Q7W286	Q7w286 bordetella
45	152.5	5.3	730	2	Q06634	Q06634 bovine herp

ALIGNMENTS

RESULT 1
Q82ER2
ID Q82ER2 PRELIMINARY; PRT; 451 AA.
AC Q82ER2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative aminotransferase.
GN OrderedLocusNames=SAV4551;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
CC -/- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent aminotransferase family.
DR EMBL; AP005039; BAC72263.1; -.
DR HSSP; P16932; 2DKB.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR Pfam; PF00202; Aminotran_3; 1.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
KW Complete proteome; Pyridoxal phosphate.
SQ SEQUENCE 451 AA; 48232 MW; 16BCAS9B276F9CA CRC64;

Query Match 9.9%; Score 284; DB 2; Length 451;
Best Local Similarity 45.9%; Pred. No. 2.3e-07;
Matches 72; Conservative 20; Mismatches 35; Indels 30; Gaps 6;
QY 1 IYSTFADRAYPGGLTYSCHPLATACAVATINAMEDGVMANARIGEOVLPGGLRLDAAR 60
DB 298 IASTFGKRAYPGGLTYSCHPLACAAAVATINVMABEGVVENAANLPGVLELAEAR 357
QY 61 HRSVGVGLGVFWAGSDPERAGLRLVEVLGAQCRRRDV---GAGDA---AAVGVGLPGQ 113

```

Db 358 HPSVGEVGVGFWA-----LELVKDRTEPLVPYNAGEANAPAAFGA----- 403
Qy 114 RQHRARADG-----SISALVASPPRAASSAPASIGL 145
Db 404 ---AAKANGLWPFINMRTHVV-PPCNVTEAEKEGL 436

RESULT 2
ID Q9XA10 PRELIMINARY; PRT; 451 AA.
AC Q9XA10;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative aminotransferase.
GN ORFNames=SC66T3.33;
CN Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
DR EMBL; AL939117; CAB45489.1; -.
DR PIR; T35390; T35390.
DR HSSP; P16932; 2DKB.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR Pfam; PF00202; Aminotran_3.1.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.
SQ SEQUENCE 451 AA; 48413 MW; 43CF2DD9AFA7E8AB CRC64;

Query Match 9.5%; Score 273; DB 2; Length 451;
Best Local Similarity 69.3%; Pred. No. 8.6e-07;
Matches 52; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 IYSTFDARAYPGGLTYSCHPLATACAVATINAMEDEGMVANARIGQVLGPGRLDLAAR 60
Db 298 IAAVFAERYPGGTYSCHPLAACAAVATINVMAEEGVVEHAARLGAEVVEPALRELAER 357
Qy 61 HRSVGEVRGLGVFWA 75
Db 358 HPSVGEVGVGTGMFWA 372

RESULT 3
ID Q8FN12 PRELIMINARY; PRT; 469 AA.
AC Q8FN12;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative aminotransferase.
GN OrderedLocusNames=CE2336;
CN Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
DR EMBL; AL939117; CAB45489.1; -.
DR PIR; T35390; T35390.
DR HSSP; P16932; 2DKB.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR Pfam; PF00202; Aminotran_3.1.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; 1.
KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.
SQ SEQUENCE 451 AA; 48413 MW; 43CF2DD9AFA7E8AB CRC64;

Query Match 9.5%; Score 273; DB 2; Length 451;
Best Local Similarity 69.3%; Pred. No. 8.6e-07;
Matches 52; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 IYSTFDARAYPGGLTYSCHPLATACAVATINAMEDEGMVANARIGQVLGPGRLDLAAR 60
Db 298 IAAVFAERYPGGTYSCHPLAACAAVATINVMAEEGVVEHAARLGAEVVEPALRELAER 357
Qy 61 HRSVGEVRGLGVFWA 75
Db 358 HPSVGEVGVGTGMFWA 372

RESULT 4
ID Q9Q5K9 PRELIMINARY; PRT; 608 AA.
AC Q9Q5K9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NTR.
OS Herpesvirus papio.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Baboon lymphocryptovirus BA65;
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,
RA Hayward G.S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF20364; AAP23950.1; -.
SQ SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;

Query Match 6.5%; Score 185.5; DB 2; Length 608;
Best Local Similarity 28.5%; Pred. No. 0.046;
Matches 109; Conservative 29; Mismatches 150; Indels 95; Gaps 22;

Qy 48 QVLGPGRLDLAARHRSVGEVRGLGVFWAGSDPERAGLRVVLGAQCRRRRDVGAGDAAAV 107
Db 44 QVHGP-----RSPRIERRGSAQRGHPFPAG-----QRPSGPTGHPAAP 84
Qy 108 GVLGPQRQHRARADGSISSALVASPPRAASSAPASIGLGPSCQHTSIHPRSSNGSPTVHI 167
Db 85 GAPGPRSPRIERRRG---SAQRGHPFPAGQRPS-----GPTGGHP-----AAPGAP---- 128

```

```

OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y8-314;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579(2003).
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent
CC aminotransferase family.
DR EMBL; AP005222; BAC19146.1; -.
DR HSSP; P12995; 1QJ3.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR Pfam; PF00202; Aminotran_3.1.
DR PROSITE; PS00600; AA TRANSFER CLASS 3; UNKNOWN_1.
KW Aminotransferase; Complete proteome; Pyridoxal phosphate; Transferase.
SQ SEQUENCE 469 AA; 50166 MW; AFP3AE4482C29F79 CRC64;

Query Match 7.1%; Score 202.5; DB 2; Length 469;
Best Local Similarity 42.7%; Pred. No. 0.0045;
Matches 41; Conservative 15; Mismatches 27; Indels 13; Gaps 1;

Qy 1 IYSTFDARAYPGGLTYSCHPLATACAVATINAMEDEGMVANARIGQVLGPGRLDLAAR 60
Db 320 IRDTFAQQYSGGLTYSCHPLAVAPALAAKVVYDEKIFERVASLGELIGRLAIGQK 379
Qy 61 HRSVGEVRGLGVFW-----AGSDPERAG 83
Db 380 YAAVGVGVGTGMFWA-----AGSDPERAG 415

RESULT 4
ID Q9Q5K9 PRELIMINARY; PRT; 608 AA.
AC Q9Q5K9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NTR.
OS Herpesvirus papio.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Baboon lymphocryptovirus BA65;
RA Zong J.-C., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,
RA Hayward G.S.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF20364; AAP23950.1; -.
SQ SEQUENCE 608 AA; 60458 MW; 4BF82ACB0A029627 CRC64;

Query Match 6.5%; Score 185.5; DB 2; Length 608;
Best Local Similarity 28.5%; Pred. No. 0.046;
Matches 109; Conservative 29; Mismatches 150; Indels 95; Gaps 22;

Qy 48 QVLGPGRLDLAARHRSVGEVRGLGVFWAGSDPERAGLRVVLGAQCRRRRDVGAGDAAAV 107
Db 44 QVHGP-----RSPRIERRGSAQRGHPFPAG-----QRPSGPTGHPAAP 84
Qy 108 GVLGPQRQHRARADGSISSALVASPPRAASSAPASIGLGPSCQHTSIHPRSSNGSPTVHI 167
Db 85 GAPGPRSPRIERRRG---SAQRGHPFPAGQRPS-----GPTGGHP-----AAPGAP---- 128

```

Query Match	6.4%;	Score 182;	DB 2;	Length 208;
Best Local Similarity	22.9%;	Pred. No. 0.24;		
Matches 152;	Conservative 65;	Mismatches 244;	Indels 204;	Gaps 36;

QY	16	YSGHPLATACATINAMEDEGVN	-----ANARIGEOVLGPGRLDAARHS-----	63
DB	141	YGRQPOQPCGGAAGAHREDGEVNGSDAHDRELSEY	-----LCSRHTTSCRTSPWS	193
QY	64	-VGEVRGLGVFWAGSDP-----	ERAGLRVVEVLGAQ--CRRDVVVGADAAAVGLGQ	113
DB	194	HVNRPPALG-----GSSNSHSDGVDRAAASSELHSQQRCRHRS	LRVYTGQSDV-----	243
QY	114	ROHRAR-ADGSISSALVASPPRAAASAPA-SITGLGPSGQHTSIHPRSSNGSPVHISQSM	171	
DB	244	--HRLGADAPASSLSESTAPVDVTSAAATAGAAAKGNERRDAPTNHSTGSGQHHQSP	301	
QY	172	NA-ASSGT-----SRRSSTLFRWQSP-----	C--MIRGSASSG-----LRESSOS	208

```
Db 302 GAVAAAGVVPSPADLANITKWKKEASSGAGGAGVGGCAHVPASATAAGNRTTTLTASAAV 361
Qy 209 ASTCTD-----GNDSGAGDQLGBFGAQQRGRKRRDRDVPAAQRPVHPAGFGPA 260
Db 362 ASGSTNEPPIIISHFGSSGGG-----GGRQRQ-----GSLVTWVSPHTHSQA 404
Qy 261 DRVCVDFGRHRRARGQHPRDGRDQASRT-VSG-----VPVESNVL SAGIRCTPTT-RA 314
Db 405 E-----EAEAHAIASELISVGGSSAPASAVPMGFTWAVFVTLSSSENSKCSPTVEFHM 460
Qy 315 VAICLATLASGVVAPOPAGDVAAAAAGSPWPV-----RSVARPVALRTGPPRRPESDT 370
Db 461 SARLSLQQQQQQPPTQPSTE-----EWPSCISGLHAERADETHDGPDAAPP--- 508
Qy 371 GSITQVGRPAVLFAPEQRCRRARDQSCRQI-----HPGGGRHVQIV---ASA 415
509 -----VHPQQQQQQGSRRLRSLTLHPLADHPQHPPARLHLQPTYRKGE 556
416 RGTVEIGSIARL-----CGKDEAVAAHVPVAVGKQYIDRALNIGPYLPAEVPAL 468
557 REGRESSSRLAATALLRSAGSTVTSSATH-----IGDELDAHYELST--PHPPASVPAS 610
469 VGSIAATG-----VPVGT-----AWIVRQYKLLRAXANWEDTWTFP 505
611 SESATASGAQATGTPPRKVPFPV-GTDNATAINELFAQAVQNTWETTRMKENL--TVLVR 667
506 SIEKHPRP-----GSVAGPVFR-----VNIGR-----AIPSRARAETHGSH 544
668 SVHEEREKRRRLQRREGSAVQRLFORVLDMSVMLRLQRTVRRIALEASSGRAADAAGWH 727
545 HHHHH 549
728 HHHHH 732

RESULT 7
Q6NMXX2
ID Q6NMXX2 PRELIMINARY; PRT; 438 AA.
AC Q6NMXX2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PLP-dependent aminotransferases (EC 2.6.1.11).
GN OrderedLocusNames=C9L2441;
OC Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
RA "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005281; BAB99834.1; -.
DR HSSP; P12995; 1QJ3.
DR GO; GO:0003992; F:acetylornithine transaminase activity; IEA.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; UNKNOWN 1.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 438 AA; 47396 MW; D6A9FF03C8D29D90 CRC64;

Query Match 6.3%; Score 180; DB 2; Length 438;
Best Local Similarity 45.3%; Pred. No. 0.064;
Matches 34; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

Qy 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGQVLPGLRLAAR 60
Db 297 IRDTFGSEAYSGGLTYSGHPLAVAPAKAALEIYAEGEIIIPRVARLGAELIEPLRLAE 356

Db 302 GAVAAAGVVPSPADLANITKWKKEASSGAGGAGVGGCAHVPASATAAGNRTTTLTASAAV 361
Qy 209 ASTCTD-----GNDSGAGDQLGBFGAQQRGRKRRDRDVPAAQRPVHPAGFGPA 260
Db 362 ASGSTNEPPIIISHFGSSGGG-----GGRQRQ-----GSLVTWVSPHTHSQA 404
Qy 261 DRVCVDFGRHRRARGQHPRDGRDQASRT-VSG-----VPVESNVL SAGIRCTPTT-RA 314
Db 405 E-----EAEAHAIASELISVGGSSAPASAVPMGFTWAVFVTLSSSENSKCSPTVEFHM 460
Qy 315 VAICLATLASGVVAPOPAGDVAAAAAGSPWPV-----RSVARPVALRTGPPRRPESDT 370
Db 461 SARLSLQQQQQQPPTQPSTE-----EWPSCISGLHAERADETHDGPDAAPP--- 508
Qy 371 GSITQVGRPAVLFAPEQRCRRARDQSCRQI-----HPGGGRHVQIV---ASA 415
509 -----VHPQQQQQQGSRRLRSLTLHPLADHPQHPPARLHLQPTYRKGE 556
416 RGTVEIGSIARL-----CGKDEAVAAHVPVAVGKQYIDRALNIGPYLPAEVPAL 468
557 REGRESSSRLAATALLRSAGSTVTSSATH-----IGDELDAHYELST--PHPPASVPAS 610
469 VGSIAATG-----VPVGT-----AWIVRQYKLLRAXANWEDTWTFP 505
611 SESATASGAQATGTPPRKVPFPV-GTDNATAINELFAQAVQNTWETTRMKENL--TVLVR 667
506 SIEKHPRP-----GSVAGPVFR-----VNIGR-----AIPSRARAETHGSH 544
668 SVHEEREKRRRLQRREGSAVQRLFORVLDMSVMLRLQRTVRRIALEASSGRAADAAGWH 727
545 HHHHH 549
728 HHHHH 732

RESULT 7
Q6NMXX2
ID Q6NMXX2 PRELIMINARY; PRT; 438 AA.
AC Q6NMXX2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PLP-dependent aminotransferases (EC 2.6.1.11).
GN OrderedLocusNames=C9L2441;
OC Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa;
RA "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005281; BAB99834.1; -.
DR HSSP; P12995; 1QJ3.
DR GO; GO:0003992; F:acetylornithine transaminase activity; IEA.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; UNKNOWN 1.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 438 AA; 47396 MW; D6A9FF03C8D29D90 CRC64;

Query Match 6.3%; Score 180; DB 2; Length 438;
Best Local Similarity 45.3%; Pred. No. 0.064;
Matches 34; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

Qy 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGQVLPGLRLAAR 60
Db 297 IRDTFGSEAYSGGLTYSGHPLAVAPAKAALEIYAEGEIIIPRVARLGAELIEPLRLAE 356
```

```
Qy 61 HRSVGEVVRGLGVFWA 75
Db 357 NVAIADVVRGIGFWA 371

RESULT 8
Q6M323
ID Q6M323 PRELIMINARY; PRT; 456 AA.
AC Q6M323;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Aminotransferase-like protein C92680.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032;
RX MEDLINE=22830027; PubMed=12948641; DOI=10.1016/S0168-1656(03)00161-5;
RA McHardy A.C., Tsuchi A., Ruckert C., Puhler A., Kalinowski J.;
RT "Genome-based analysis of biosynthetic aminotransferase genes of
RT Corynebacterium glutamicum.";
RL J. Biotechnol. 104:229-240(2003).
DR EMBL; AY238324; AA092315.1; -.
DR HSSP; P12995; 1QJ3.
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; UNKNOWN 1.
KW Aminotransferase; Transferase.
SQ SEQUENCE 456 AA; 49372 MW; FEASE064E66195AE CRC64;

Query Match 6.3%; Score 180; DB 2; Length 456;
Best Local Similarity 45.3%; Pred. No. 0.067;
Matches 34; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

Qy 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGQVLPGLRLAAR 60
Db 315 IRDTFGSEAYSGGLTYSGHPLAVAPAKAALEIYAEGEIIIPRVARLGAELIEPLRLAE 374

Qy 61 HRSVGEVVRGLGVFWA 75
Db 375 NVAIADVVRGIGFWA 389

RESULT 9
Q6M323
ID Q6M323 PRELIMINARY; PRT; 456 AA.
AC Q6M323;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Aminotransferase class-III, pyridoxal-phosphate dependent.
GN CRFNames=C92680;
OS Corynebacterium glutamicum ATCC 13032.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=196627;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 20300;
RX MEDLINE=22830012; PubMed=12948626; DOI=10.1016/S0168-1656(03)00154-8;
RA Kalinowski J., Bathe B., Bartels D., Bischoff N., Bott M.,
RA Burkowski A., Dusch N., Eggeling L., Birkmanns B.J., Gaigalat L.,
RA Goemann A., Hartmann M., Hutmacher K., Kramer R., Linke B.,
RA McHardy A.C., Meyer F., Mockel B., Pfeifferle W., Puhler A., Rey D.A.,
RA Ruckert C., Rupp O., Sahn H., Wendisch V.F., Wiesgrabe I., Tsuchi A.;
RT "The complete Corynebacterium glutamicum ATCC 13032 genome sequence
RT and its impact on the production of L-aspartate-derived amino acids
RT and vitamins.";
```

```

RL J. Biotechnol. 104:5-25(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 20300;
RA Kalinowski J.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX927155; CAF21103.1;
DR GO; GO:0030170; F:pyridoxal phosphate binding; IEA.
DR GO; GO:0008483; F:transaminase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR005814; AminoTrans_3
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; UNKNOWN_1.
KW AminoTransferase; Transferase.
SQ SEQUENCE 456 AA; 49372 MW; FEA5E064E66195AE CRC64;

Query Match 6.3%; Score 180; DB 2; Length 456;
Best Local Similarity 45.3%; Pred. No. 0.067;
Matches 34; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

Qy 1 IYSTPADRAYPGGLTYSYGHPLATACAVATINAMEDGMVANAARIGEQVLGRLDLAAR 60
315 IRTDFGSEAYSGGLTYSYGHPLAVAPAKAALAIYAGEIIPRVARLGAELIEPRLELAEE 374
Qy 61 HRSVGEVGLGVFWA 75
: : : : :
Db 375 NVAIADVRGIGFFWA 389

RESULT 10
Q6X125 PRELIMINARY; PRT; 1408 AA.
ID Q6X125
AC Q6X125;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE BiCP4 positive and negative gene regulator.
GN ORFName=BHV5-61, BHV5-72;
OS Bovine herpesvirus 5.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=35244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SV507/99;
RX MEDLINE=22850801; PubMed=12970418;
RX DOI=10.1128/JVI.77.19.10339-10347.2003;
RA Delhon G.F., Moraes M.P., Lu Z., Afonso C.L., Flores E.F., Weiblen R.,
RA Kutish G.F., Rock D.L.;
RT "Genome of bovine herpesvirus 5.";
EMBL; AY261359; AAR86178.1;
EMBL; AY261359; AAR86167.1;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR005205; Herpes_ICP4_C.
DR InterPro; IPR005206; Herpes_ICP4_N.
DR Pfam; PF03585; Herpes_ICP4_C; 1.
DR Pfam; PF03584; Herpes_ICP4_N; 1.
SQ SEQUENCE 1408 AA; 141784 MW; 90508869D9CED687 CRC64;

Query Match 6.3%; Score 179.5; DB 2; Length 1408;
Best Local Similarity 21.3%; Pred. No. 0.22;
Matches 148; Conservative 55; Mismatches 212; Indels 279; Gaps 32;

Qy 3 STPADRAYPGGLTYSYGHPLATACAVATINAMEDGMVANAARIGEQVLGPG 53
: : : : :
Db 467 AVLGAAPAPLPPAPGPAARERLRELACCAACREALE-----AARCAAGAGSGG 519

Qy 54 LRDIAAHRHSVGEVGLGVFWAGSD-----PERAGLRVEVLGACRRDVRVVGADAAVG 108
: : : : :
Db 520 ASELPLVSLAAG--RGLPAAACAPDALAAHPERVIRAAELIGA---ARDAV----- 565

```



```
QY 334 GDVARA-----AAAGSPWVRVSRP-----VAVLRGTPPPRRPSDTGCSITQVGRP 379
Db 439 ASSASATSSAAASAPAPAPAPRRKRSTNNHLSLMADGPP---PTDGLPLTLGEP 495
QY 380 AVLFAPEQRCRRRA-----DQSCROIHPGGGRHVQIVASAGTV-----EIGS 423
Db 496 WFGSDPPADGVRVRYGAGDSREGLWDEDVQ-----AAARY-----RAAAGPVFVPIPEMGD 548
QY 424 IARLCGKDEAAALHYVAPVGEKQDYID-----RALRNIQPYLPAP 464
Db 549 SRK-----QHEALVRLIYSGAAGMSWLNQPMQADQRFNQCQRRVHAPHGHSFITGS 605
QY 465 V-----PALVGSIAATGPGVTAWIVROYPKLLRAKANMEDTWTFFSIEKEHPRGVSAGP 520
Db 606 VTPPLPHIGDAMAQDPL-----WALPHAVASAVMSRRYDRTQTKFILQSLRRAYADWAP 661
QY 521 VFRVNLGRAIPSRARA 537
Db 662 -----GRAADPRAGEA 672

Query Match
Best Local Similarity 24.2%; Pred. No. 1.2; Length 3889;
Matches 116; Conservative 49; Mismatches 190; Indels 124; Gaps 22;

QY 33 MEDEGMVANAARIQEVQLPGGLRLDAKRRSVGEVGLGVFWAGSDPERAGLRYEVLGAQ 92
Db 2802 MEDE-----AAATRIQDAAADPAVEANRRSRKQAGSV-----EEQVAINPMAVPRAS 2849
QY 93 CRRDVRVCGAADAAGVGLGQRRARADGSGISSALVALSPRAASAPASIGLPGSQHT 152
Db 2850 VLERPDVAASLAANA-----ASGAPPGQTGPLPITTEATGEN-----GLGSS----- 2892
QY 153 SIHPRSSNGSPVTHISQSMNAASGTSRRSTLFRWQS--PCMIPGSGASSGLRESSOSAS 210
Db 2893 ---PRDGRVMTTASVSHGRD-----TSKLLHPMAPRSLGASLVPASATT-----NGSGN 2940
QY 211 TCTDNGDSGAGSDOLGEGPAQQRGRHRRDRDVPAAQORPAVHPAGPGPADRVGVDPGRH 270
Db 2941 SSGNGREGSGSTSGGAPAMPERR-----VGGAPSNASAAAAA-----AQPAAH 2991
QY 271 RRARGQHOPRGSQRQASRTVSGVFPVSNVLASGIRCKTPPTTRVAICLATLASR-GVWA 329
Db 2992 QDLFG-----ELDTTTLTTSKMTADAGAAAPPNLPSPMWR-----LGSRLGLVR 3035
QY 330 PQPADGVARAAAAGSPWVRVSRPVAVLRTGTPPPRRPSDTGSIQVGRPAVLPAPEQR 389
```

```
Db 3036 GGSNSGAQVAPA-SPLPAKAPSPAAAARPP-----GAVTT--NAAVPMPPQKV 3085
QY 390 RRR-----ADQSCROIHP-----GGGRH-----VOIVASARGTVEIGSIARLCGKDE 432
Db 3086 FRSPSEFANARQAAPPAAPAAAANGGRELKQOPAVQAVSSTTSIRSNS-----SGSGN 3141
QY 433 AVAALHYVAPVGEKQDYIDRALRNIQPYLPAPVPAVPAVGVGIA-----ATGPPVPGTAW 483
Db 3142 PLA-----RALRYMSVPKPGQAPSTASNAAPAAAABEAPAPPSRHTAW 3184

RESULT 14
RAA3_CHLRE
ID _RAA3_CHLRE STANDARD; PRT; 1783 AA.
AC Q9FEC4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Trans-splicing factor Raa3, chloroplast precursor.
GN Name=RAA3;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
[1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP STRAIN=137c / CC-125;
RX MEDLINE=21181833; PubMed=11285239; DOI=10.1093/emboj/20.7.1765;
RA Rivier C., Goldschmidt-Clermont M., Rochaix J.-D.;
RT "Identification of an RNA-protein complex involved in chloroplast
group II intron trans-splicing in Chlamydomonas reinhardtii.";
RL EMBO J. 20:1765-1773(2001).
CC -!- FUNCTION: Required for trans-splicing of exons 1 and 2 of the
chloroplast encoded psaa mRNA (a group II intron). May be required
for stability of the chloroplast RNA-protein complex in which it
is found.
CC -!- SUBUNIT: Part of a 1700 kDa complex that includes the precursor
RNA to exon 1 and the tscA RNA.
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma.
CC -!- DOMAIN: The N-terminal 453 amino acids are dispensable, while the
C-terminal 630 amino acids are required for function.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; AF310675; AAC40000.1; -
CC EMBL; AF310674; AAG39999.1; -
CC EMBL; AF310673; AAG39999.1; -
CC TRANSIT 1 40
CC CHAIN 41 1783
CC DOMAIN 112 311
CC DOMAIN 343 436
CC DOMAIN 478 1078
CC DOMAIN 1310 1415
CC DOMAIN 1416 1430
CC DOMAIN 1496 1506
CC DOMAIN 1678 1722
CC DOMAIN 771 778
CC DOMAIN 920 926
CC DOMAIN 927 932
CC DOMAIN 1047 1055
CC DOMAIN 1318 1325
CC DOMAIN 1405 1415
CC DOMAIN 1669 1675
CC SEQUENCE 1783 AA; 180399 MW; 40F6206BAGEBDCDB CRC64;

Query Match
6.1%; Score 174; DB 2; Length 3889;
Best Local Similarity 24.2%; Pred. No. 1.2;
Matches 116; Conservative 49; Mismatches 190; Indels 124; Gaps 22;

QY 33 MEDEGMVANAARIQEVQLPGGLRLDAKRRSVGEVGLGVFWAGSDPERAGLRYEVLGAQ 92
Db 2802 MEDE-----AAATRIQDAAADPAVEANRRSRKQAGSV-----EEQVAINPMAVPRAS 2849
QY 93 CRRDVRVCGAADAAGVGLGQRRARADGSGISSALVALSPRAASAPASIGLPGSQHT 152
Db 2850 VLERPDVAASLAANA-----ASGAPPGQTGPLPITTEATGEN-----GLGSS----- 2892
QY 153 SIHPRSSNGSPVTHISQSMNAASGTSRRSTLFRWQS--PCMIPGSGASSGLRESSOSAS 210
Db 2893 ---PRDGRVMTTASVSHGRD-----TSKLLHPMAPRSLGASLVPASATT-----NGSGN 2940
QY 211 TCTDNGDSGAGSDOLGEGPAQQRGRHRRDRDVPAAQORPAVHPAGPGPADRVGVDPGRH 270
Db 2941 SSGNGREGSGSTSGGAPAMPERR-----VGGAPSNASAAAAA-----AQPAAH 2991
QY 271 RRARGQHOPRGSQRQASRTVSGVFPVSNVLASGIRCKTPPTTRVAICLATLASR-GVWA 329
Db 2992 QDLFG-----ELDTTTLTTSKMTADAGAAAPPNLPSPMWR-----LGSRLGLVR 3035
QY 330 PQPADGVARAAAAGSPWVRVSRPVAVLRTGTPPPRRPSDTGSIQVGRPAVLPAPEQR 389
```

```

Best Local Similarity 21.1%; Pred. No. 0.57;
Matches 127; Conservative 64; Mismatches 235; Indels 177; Gaps 22;

Qy 13 GLTYSGLPLATACAVATINAMEDSGMVANARIGEQLVGLPGLRLDLAARHRS-----VGEV 67
Db 118 QOARHRRQMAAATTVSAAPQTGATKPAATAXTTTPQPRGSDADAGSAQSQYGFDP 177
Qy 68 RGLGVF-----WAGSDPERAGLVEVLGAQC--RRRDVVG-----AGDAAVG 108
Db 178 PGGGALKAVDAASDAADPVAASAPAGISDQLSTPACPPERPQAKPRASRAPAAP 237
Qy 109 VLGPQ-----ROHARA-DGSI-----SALVSPPPRAASSAP 140
Db 238 GVGFQDVGGSGACAPAPDESHMGLTHRDQGHDERISQTAGEAKKACAVAPPAPTSP 297
Qy 141 ASIGLGP-----SQGHTSIH 155
Db 298 PGLAAAPTRLASSALGTHSSDGMRRRAVPGRTDPSLSAVAGPVTLSGSSSSSGRNSN 357
Qy 156 PRSNGSPTHVHSQSMNAASGTS-----RRSSTLFRWQS-----PC 192
Db 358 SNTSTSTSGVTITTSNVGNGASPOBELMAARRAVVTMQNTHLGRGRSPAPLPTGGM 417
Qy 193 MIPGSASSGLRESSQASTCTDGNDSGAGSD-OLGEPGAQORQRKHRRDRVPAQORPA 251
Db 418 SIATSAASSSTSSASSSSMNDGNAKTSDAVSLPVGQ-----PAEQPH 465
Qy 252 VHPAGPGADRVGVDPGHRRARQHQHPRDGSRDQASRTVSG-----VPVESNLS 302
Db 466 V-PTAPGPGSQTGAS-----AVAAQAPSSAMPTAAMAATMGSAATLPTAAVSS 518
Qy 303 AGTCRTPTTTRAVAILATLASRGAQAGDVARAAAAGSPVPSVARPVAVLETGP 362
Db 519 AAEGTQPSGLLAGGRPALGRTI-----QGRITARLOAAREALRAARHARVGAAMQPPP 573
Qy 363 PPRRP--SDTGSITQVGRPAVLFAPEQRCRRRQDQSCROIHPGCGGRHVQIVASARGTVE 420
Db 574 VQARPVGQSGVQVQGVQSPGQ-----RRQEPAAATKLHVADGLPARPVQPAVSATD 630
Qy 421 IGSTARLCGKDEAAVLAHYVAPVGEKQDYIDRALRNIGPYLPAEVPAVGVSGIA-ATGPVP 479
Db 631 LQT-----DTATAA-SAPFPVSD-----ASLGSTELAASAPTTSLASAGPAI 673
Qy 480 GTA 482
Db 674 GTS 676

RESULT 15
IE18 PRVKA
ID IE18 PRVKA STANDARD; PRT; 1446 AA.
AC P33479;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Immediate-early protein IE180.
GN Name=IE;
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=33703;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021039; PubMed=2171211;
RA Vitek C., Kozmik Z., Paces V., Schirm S., Schwytzer M.;
RT "Pseudorabies virus immediate-early gene overlaps with an oppositely
RT oriented open reading frame: characterization of their promoter and
RT enhancer regions."
RL Virology 179:365-377 (1990).
CC -!- FUNCTION: This IE protein is a multifunctional protein capable of
CC migrating to the nucleus, binding to DNA, trans-activating other
CC viral genes, and autoregulating its own synthesis.
CC -!- SUBCELLULAR LOCATION: Nucleus of infected cells.

```

```

-!- PTM: A long stretch of serine residues may be a major site of
phosphorylation.
-!- SIMILARITY: Belongs to the herpesviruses ICP4/IE140/IE180 family.
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
EMBL; M34651; AAA47470.1; -.
PIR; A45344; A45344.
InterPro; IPR005205; Herpes ICP4 C.
InterPro; IPR005206; Herpes ICP4 N.
Pfam; PF03585; Herpes ICP4 C; 1.
Pfam; PF03584; Herpes ICP4 N; 1.
DNA-binding; Early protein; Nuclear protein; Phosphorylation;
Trans-acting factor; Transcription regulation.
FT DOMAIN 347 354 Poly-Ser.
FT DOMAIN 379 397 Poly-Ser.
SQ SEQUENCE 1446 AA; 148640 MW; 81P43A3DE3DDA068 CRC64;

Query Match 6.0%; Score 172; DB 1; Length 1446;
Best Local Similarity 21.3%; Pred. No. 0.56;
Matches 154; Conservative 54; Mismatches 224; Indels 290; Gaps 31;

Qy 27 VATINAMEDEGMVANAARIGEQLVGLPGLRLDLAARHRS-SVGEVRLGLVFWAGSDPERAGLR 85
Db 19 LAAAAAAEEGSIAS-----GPDGSGSRRRSGSGEDLLFGPGLFSD-DAAEAE 67
Qy 86 VEVLGAQRRRRDVGAGDAAAACVGLGP-----QOHRARADGSI-----S 125
Db 68 AAVL-----AAAAGATPRPPPSAQOQQQPPRGSGEIVLWDEDEDEPG 113
Qy 126 SALVAPPPRAASAPASIGLPGSGQHTSIHPRSSNGS---PTVHISQSMNAASSTSR 181
Db 114 SPAGSPGARA-----LHQGSEHGLVLPGRSRAGSGRPPTPPAALAAAGACGPGGR 166
Qy 182 SSTLFRWQSPFCMIPGSASSGLRESSQASTCTDGNDSGAGSDQLGEPGAQORQRKHDR 241
Db 167 SSP-----SAASPASSSGSPGSPSAAPRRWSPARGDPVGEPPGAARPTPAPPA 214
Qy 242 RD-----VPAQORPAVHPAGP-----GPADRVGVDPGRH-----R 271
Db 215 QPAAVAAAPARRGPA-SPASPAAGPVSPAGGGGAPSGAGGDRGHHHQHREPLDEPAAAR 273
Qy 272 R-----ARG-----OHQPR-- 280
Db 274 RLDPRLGARSVPSSNPNSNSNTTAVETVARGPEKDEDEGLGLAGDGGAPPQRP 333
Qy 281 -----DGSD-----RQASRTVSGVPVESNLS 302
Db 334 RAGEGALRRGRGFSSSSSGSDLSPARSPAPAPAAARSAASSSSSSSSSSSSSS 393
Qy 303 A-----GIRCTPTTTRAVAILATLASRG-----VVAPOPAGDVAAAAAGSP 345
Db 394 SSSSEGEDEGVKPGAPLARA-----GPPSPAPAPAAAPRPSASSASSAAASP 442
Qy 346 WPVRSVARP-----VAVLRTGPPPRPSDTGSIQVGRPAVLFAPEQRCRRRA- 393
Db 443 APAPEPARPRKRRTNNHLSLMADGPP---PTDGLTLPTEGFWGSDPPADGRVRYG 499
Qy 394 -----DQSCRQIHPGGRHVQIVASARGTV-----EIGSTARLCGKDEAAVLAH 438
Db 500 GAGDSREGLWDEDDVRQ---AAARY---RAAAGPVVFIPEMGDSRK---QHEALVRLI 549
Qy 439 YVAPVCEKQDYD-----RALRNI GPYLPAPV-----PALVGSIAAT 475
Db 550 YSGAAGEAMSWLQNPQMOPADQRFNOCORRVHAPHGHSGFITGVTPLPHITGDMAAQ 609
Qy 476 GPVPGTAVIVRQYPKLLRAKANWEDTWTFFPSEKHRPRGVSAGPVFRVNLGRAIPSRAA 535

```

Db	610	DPL----	WALPHA	SAVAMS	REYDR	TQKTF	ILQSL	RRAYAD	MAYP-----	GRAAD	PRAG	659
Qy	536	RA	537									
Db	660	EA	661									

Search completed: September 16, 2005, 20:52:08
Job time : 184 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:27:42 ; Search time 25 Seconds
(without alignments)
1639.293 Million cell updates/sec

Title: US-10-607-752-116

Perfect score: 2862

Sequence: 1 IYSTFADRAYPGGLTYSVGH...IPSRARAAEIHGSHHHHH 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Minimum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2862	100.0	582	3	US-09-450-072-81
2	2862	100.0	582	4	US-09-351-348-81
3	2145	74.9	582	3	US-09-450-072-80
4	2145	74.9	582	4	US-09-351-348-80
5	1906	66.6	582	3	US-09-450-072-79
6	1906	66.6	582	4	US-09-450-072-79
7	490	17.1	97	3	US-09-450-072-71
8	490	17.1	97	4	US-09-351-348-71
9	440	15.4	87	3	US-09-450-072-74
10	440	15.4	87	4	US-09-351-348-74
11	389	13.6	75	3	US-09-450-072-70
12	389	13.6	75	4	US-09-351-348-70
13	373	13.0	70	3	US-09-450-072-69
14	373	13.0	70	4	US-09-351-348-69
15	326	11.4	59	3	US-09-450-072-77
16	326	11.4	59	4	US-09-351-348-77
17	255	8.9	49	3	US-09-450-072-72
18	255	8.9	49	4	US-09-351-348-72
19	237	8.3	46	3	US-09-450-072-73
20	237	8.3	46	4	US-09-351-348-73
21	224	7.8	44	3	US-09-450-072-76
22	224	7.8	44	4	US-09-351-348-76
23	222	7.8	456	4	US-09-489-039A-13165
24	206	7.2	38	3	US-09-450-072-67
25	206	7.2	38	4	US-09-351-348-67
26	204.5	7.1	819	4	US-09-252-991A-19569
27	196.5	6.9	606	4	US-09-252-991A-18233

28	196	6.8	613	4	US-09-252-991A-22424	Sequence 22424, A
29	194	6.8	973	4	US-09-252-991A-21386	Sequence 21386, A
30	192	6.7	802	4	US-09-252-991A-25050	Sequence 25050, A
31	191.5	6.7	672	4	US-09-252-991A-16941	Sequence 16941, A
32	191.5	6.7	1037	4	US-09-252-991A-25361	Sequence 25361, A
33	190.5	6.7	618	4	US-09-252-991A-23373	Sequence 23373, A
34	190.5	6.7	957	4	US-09-252-991A-20408	Sequence 20408, A
35	189.5	6.6	588	4	US-09-252-991A-30690	Sequence 30690, A
36	186	6.5	726	4	US-09-252-991A-20675	Sequence 20675, A
37	185	6.5	1246	4	US-09-252-991A-23140	Sequence 23140, A
38	180.5	6.3	412	4	US-09-252-991A-23193	Sequence 23193, A
39	180.5	6.3	822	4	US-09-252-991A-22479	Sequence 22479, A
40	180.5	6.3	1706	4	US-09-252-991A-31760	Sequence 31760, A
41	180	6.3	757	4	US-09-252-991A-23569	Sequence 23569, A
42	179	6.3	32	3	US-09-450-072-65	Sequence 65, Appl
43	179	6.3	32	4	US-09-351-348-65	Sequence 65, Appl
44	178.5	6.2	420	4	US-09-252-991A-20033	Sequence 20033, A
45	177.5	6.2	703	4	US-09-252-991A-31954	Sequence 31954, A

ALIGNMENTS

RESULT 1
US-09-450-072-81

; Sequence 81, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
; US-09-450-072-81

Query Match	100.0%	Score 2862;	DB 3;	Length 582;
Best Local Similarity	100.0%	Pred. No. 4.9e-241;		
Matches 549;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	IYSTFADRAYPGGLTYSVGHPLATACAVATINAMEDGVANAARIGEQLGFLDLAAR	60	
Db	34	IYSTFADRAYPGGLTYSVGHPLATACAVATINAMEDGVANAARIGEQLGFLDLAAR	93	
QY	61	HRSGVEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAVAAGVLPQQRHARA	120	
Db	94	HRSGVEVRLGVFWAGSDPERAGLRVEVLGAQCRDRDVGAGDAVAAGVLPQQRHARA	153	
QY	121	DGSISSALVAPPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNNAASSGTSR	180	
Db	154	DGSISSALVAPPPRAASSAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNNAASSGTSR	213	
QY	181	RSSTLFRWQSCMTPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKGRD	240	
Db	214	RSSTLFRWQSCMTPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEPGAQQRQKGRD	273	
QY	241	RDDVPAQQRPAVHAGPGPADRVGVDFGRHRRARQHQPRGSDRQASRTVSGVPVSNV	300	
Db	274	RDDVPAQQRPAVHAGPGPADRVGVDFGRHRRARQHQPRGSDRQASRTVSGVPVSNV	333	
QY	301	LSAGIRCKTPTTTRAVAICLATLASRGVVVAPOPAGDVARAAAAGSPVRSVARPVAVLRT	360	
Db	334	LSAGIRCKTPTTTRAVAICLATLASRGVVVAPOPAGDVARAAAAGSPVRSVARPVAVLRT	393	

Qy 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 420
Dd 394 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 453
Qy 421 IGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
Dd 454 IGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 513
Qy 481 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSAARAABI 540
Dd 514 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSAARAABI 573
Qy 541 HGSHHHHH 549
Dd 574 HGSHHHHH 582

RESULT 2
US-09-351-348-81
; Sequence 81, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: Of Mycobacterial Infections with Multi-Epitope Vaccines
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351.348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab

US-09-351-348-81
Query Match 100.0%; Score 2862; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 4.9e-241;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEVLGPGRLDLAAR 60
Dd 34 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEVLGPGRLDLAAR 93
Qy 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRERDVVGAGDAAAVGLGPGRQHRARA 120
Dd 94 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRERDVVGAGDAAAVGLGPGRQHRARA 153
Qy 121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
Dd 154 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 213
Qy 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDNDGSGSDQLGEPGAQRQGRKRD 240
Dd 214 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDNDGSGSDQLGEPGAQRQGRKRD 273
Qy 241 RRDVPAQRPAVHPAGPADRVGDPGRHRRARGQHPRDSRQASRTVSGVPVPSNV 300
Dd 274 RRDVPAQRPAVHPAGPADRVGDPGRHRRARGQHPRDSRQASRTVSGVPVPSNV 333
Qy 301 LSAGIRCTPTTTRAVAI CLATLASRGVVAPOPAGDVARAAAAGSPWVRVARPVAVLRT 360
Dd 334 LSAGIRCTPTTTRAVAI CLATLASRGVVAPOPAGDVARAAAAGSPWVRVARPVAVLRT 393
Qy 361 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 420
Dd 394 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 453
Qy 421 IGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480

Dd 454 IGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 513
Qy 481 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSAARAABI 540
Dd 514 TAWIVROYPKLLRAKANWEDTWTFFSIEEKHPRGSGVAGPVFRVNLGRAIPSAARAABI 573
Qy 541 HGSHHHHH 549
Dd 574 HGSHHHHH 582

RESULT 3
US-09-450-072-80
; Sequence 80, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450.072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351.348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab

US-09-450-072-80
Query Match 74.9%; Score 2145; DB 3; Length 582;
Best Local Similarity 67.4%; Pred. No. 1.6e-178;
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

Qy 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEVLGPGRLDLAAR 60
Dd 34 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEVLGPGRLDLAAR 93
Qy 61 HRSVGEVRGLGVFWAGSDPERAGLVEVLGAQCRERDVVGAGDAAAVGLGPGRQHRARA 120
Dd 94 HRSVGEVRGLGVFWA----- 108
Qy 121 DGSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
Dd 109 -GSISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 167
Qy 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDNDGSGSDQLGEPGAQRQGRKRD 240
Dd 168 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDNDGSGA----- 207
Qy 241 RRDVPAQRPAVHPAGPADRVGDPGRHRRARGQHPRDSRQASRTVSGVPVPSNV 300
Dd 208 -----GSDRQASRTVSGVPVPSNV 226
Qy 301 LSAGIRCTPTTTRAVAI CLATLASRGVVAPOPAGDVARAAAAGSPWVRVARPVAVLRT 360
Dd 227 LSAGIRCTPTTTRAVAI CLATLASRGVVAPOPAGDVARAAAAGSPWVRVARPVAVLRT 286
Qy 361 GPPRRPSDT----- 370
Dd 287 GPPRRPSDTSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTV 346
Qy 371 -----GSTTQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTV 419
Dd 347 RRARGQHPRDSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTV 406
Qy 420 EIGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNIGPYLPAEVPALV----- 469
Dd 407 EIGSIARLCGKDEAVALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSDDPERAGLR 466

QY 470 -----GSIAATGVPVGTAWIVROYPKLLR 493
DB 467 VEVLGAQCRRRDVVVGADAAAVGLGQROHRAADGSIATGTPVGTAWIVROYPKLLR 526
QY 494 AKANWEDTWTFFSIEEKHPRGSGVAGPVFVNVLGRAIPSRARAABEIHGSHHHH 549
DB 527 AKANWEDTWTFFSIEEKHPRGSGVAGPVFVNVLGRAIPSRARAABEIHGSHHHH 582

RESULT 5
US-09-450-072-79
; Sequence 79, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcavre, Alain
; TITLE OF INVENTION: Compounds for Treatment
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-351-348-80

Query Match 74.9%; Score 2145; DB 4; Length 582;
Best Local Similarity 67.4%; Pred. No. 1.6e-178;
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLPGLDLAAR 60
DB 34 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLPGLDLAAR 93
QY 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRRRDVVVGADAAAVGLGQROHRAA 120
DB 94 HRSVGEVRLGVFWA----- 108
QY 121 DGSISSALVASPPRAASAPASIGLPSQHTSIHPRSSNGSPTVHISQSMNAASGTSR 180
DB 109 -GSISSALVASPPRAASAPASIGLPSQHTSIHPRSSNGSPTVHISQSMNAASGTSR 167
QY 181 RSSTLFRWQSPCMIPGSASSGLRESQSASTCTDGNDSGAGSDQLGEPGAQORQKH 240
DB 168 RSSTLFRWQSPCMIPGSASSGLRESQSASTCTDGNDSGA----- 207
QY 241 RRDVPAQORPAVHPAGPGPADRVGDPGRHRRARQHQPRDGSDDQASRTVSGVPESNV 300
DB 208 -----GSDQASRTVSGVPESNV 226
QY 301 LSAGIRCRPTTTTRAVAIATLASRGVAPQAGDVARAAAAGSPWVRSVARPVAVLRT 360
DB 227 LSAGIRCRPTTTTRAVAIATLASRGVAPQAGDVARAAAAGSPWVRSVARPVAVLRT 286
QY 361 GPPRRPSDT----- 370
DB 287 GPPRRPSDTGSDQLGEPGAQORQKHRRDRDVPAAQORPAVHPAGPGPADRVGDPGRH 346
QY 371 -----GSIITQVGRPAVLFAPEQRCRRADORSCTHPCGGGRHVQIVASARGTV 419
DB 347 RRARQHQPRDGSITQVGRPAVLFAPEQRCRRADORSCTHPCGGGRHVQIVASARGTV 406
QY 420 EIGSTARLCGKDEAAVAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALV----- 469
DB 407 EIGSTARLCGKDEAAVAALHYVAPVGEKQYIDRALRNIGPYLPAEVPALVGSDDPERAGIR 466
QY 470 -----GSIAATGVPVGTAWIVROYPKLLR 493

DB 467 VEVLGAQCRRRDVVVGADAAAVGLGQROHRAADGSIATGTPVGTAWIVROYPKLLR 526
QY 494 AKANWEDTWTFFSIEEKHPRGSGVAGPVFVNVLGRAIPSRARAABEIHGSHHHH 549
DB 527 AKANWEDTWTFFSIEEKHPRGSGVAGPVFVNVLGRAIPSRARAABEIHGSHHHH 582

RESULT 5
US-09-450-072-79
; Sequence 79, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcavre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorder
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1042cl
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-450-072-79

Query Match 66.6%; Score 1906; DB 3; Length 582;
Best Local Similarity 57.1%; Pred. No. 1.1e-157;
Matches 399; Conservative 0; Mismatches 0; Indels 300; Gaps 2;

QY 1 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLPGLDLAAR 60
DB 34 IYSTFADRAYPGGLTYSYGHPLATACAVATINAMEDEGMVANAARIGEQLVGLPGLDLAAR 93
QY 61 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRRRDVVVGADAAAVGLGQROHRAA 120
DB 94 HRSVGEVRLGVFWAGSDPERAGLRVEVLGAQCRRRDVVVGADAAAVGLGQROHRAA 153
QY 121 ----- 120
DB 154 DGSDDQASRTVSGVPESNVLSAGIRCRPTTTTRAVAIATLASRGVAPQAGDVARAA 213
QY 121 ----- 120
DB 214 AAGSPWVRSVARPVAVLRTGPPRRRSDTGTGDLGEPGAQORQKHRRDRDVPAAQORP 273
QY 121 -----DGSISSALVASPPRAASAPASIGLPSQ 150
DB 274 AVHPAGPGPADRVGDPGRHRRARQHQPRDGSISSALVASPPRAASAPASIGLPSQ 333
QY 151 HTSIHPRSSNGSPTVHISQSMNAASGTSRSTLFRWQSPCMIPGSASSGLRESQSAS 210
DB 334 HTSIHPRSSNGSPTVHISQSMNAASGTSRSTLFRWQSPCMIPGSASSGLRESQSAS 393
QY 211 TCTDGNDSGAGSDQLGEPGAQORQKHRRDRDVPAAQORPAVHPAGPGPADRVGDPGRH 270
DB 394 TCTDGNDSGA----- 403
QY 271 RRARQHQPRDGSDDQASRTVSGVPESNVLSAGIRCRPTTTTRAVAIATLASRGVAP 330
DB 404 ----- 403
QY 331 OPAGDVARAAAAGSPWVRSVARPVAVLRTGPPRRRSDTGTGDLGEPGAQORQKHRRDRDVPAAQORP 390
DB 404 -----GSIITQVGRPAVLFAPEQRCR 423
QY 391 RRADORSCTHPCGGGRHVQIVASARGTVETIGSTARLCGKDEAAVAALHYVAPVGEKQYI 450
DB 424 RRADORSCTHPCGGGRHVQIVASARGTVETIGSTARLCGKDEAAVAALHYVAPVGEKQYI 483


```
|||||
Db 61 TLFRTWSPICPGSASSGLRESSQSASTCTDGNDSGA 97

RESULT 9
US-09-450-072-74
; Sequence 74, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT FILING DATE: 1999-11-29
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-450-072-74

Query Match 15.4%; Score 440; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 5.2e-31;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 DRQASRTVSGVPVSVNLVLSAGIRCRPTTTRAVAICLATLASRGVVAPOAGDVAAAAAG 343
Db 1 DRQASRTVSGVPVSVNLVLSAGIRCRPTTTRAVAICLATLASRGVVAPOAGDVAAAAAG 60
QY 344 SPWPVRSVARPVAVLRTGPPRRPSDT 370
Db 61 SPWPVRSVARPVAVLRTGPPRRPSDT 87

RESULT 10
US-09-351-348-74
; Sequence 74, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; FILE REFERENCE: 11000.1042
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-351-348-74

Query Match 15.4%; Score 440; DB 4; Length 87;
Best Local Similarity 100.0%; Pred. No. 5.2e-31;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 DRQASRTVSGVPVSVNLVLSAGIRCRPTTTRAVAICLATLASRGVVAPOAGDVAAAAAG 343
Db 1 DRQASRTVSGVPVSVNLVLSAGIRCRPTTTRAVAICLATLASRGVVAPOAGDVAAAAAG 60
QY 344 SPWPVRSVARPVAVLRTGPPRRPSDT 370
Db 61 SPWPVRSVARPVAVLRTGPPRRPSDT 87

RESULT 11
US-09-450-072-70
; Sequence 70, Application US/09450072
```

```
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT FILING DATE: 1999-11-29
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-450-072-70

Query Match 13.6%; Score 389; DB 3; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDGVMVANAARIGEVLGFLRDLAAR 60
Db 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDGVMVANAARIGEVLGFLRDLAAR 60
QY 61 HRSVGEVRGLGVFWA 75
Db 61 HRSVGEVRGLGVFWA 75

RESULT 12
US-09-351-348-70
; Sequence 70, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; FILE REFERENCE: 11000.1042
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-351-348-70

Query Match 13.6%; Score 389; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDGVMVANAARIGEVLGFLRDLAAR 60
Db 1 IYSTPADRAYPGGLTYSGHPLATACAVATINAMEDGVMVANAARIGEVLGFLRDLAAR 60
QY 61 HRSVGEVRGLGVFWA 75
Db 61 HRSVGEVRGLGVFWA 75

RESULT 13
US-09-450-072-69
; Sequence 69, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; FILE REFERENCE: 11000.1042c1
; CURRENT FILING DATE: 1999-07-12
```

```
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-450-072-69

Query Match      13.0%; Score 373; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 IAATGVPGTATVIRQYPKLLRAKANWEDTTFPSIEEKHRPRGSGVAGPVFRVNLGRAIP 531
|||||
1 IAATGVPGTATVIRQYPKLLRAKANWEDTTFPSIEEKHRPRGSGVAGPVFRVNLGRAIP 60

QY 532 SRAARAAEIH 541
|||||
61 SRAARAAEIH 70

Db

RESULT 14
US-09-351-348-69
; Sequence 69, Application US/09351348
; Patent No. 6436898
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Mycobacterial Infections with Multi-Epitope Vaccines
; FILE REFERENCE: 11000.1042
; CURRENT APPLICATION NUMBER: US/09/351,348
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-351-348-69

Query Match      13.0%; Score 373; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.7e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 472 IAATGVPGTATVIRQYPKLLRAKANWEDTTFPSIEEKHRPRGSGVAGPVFRVNLGRAIP 531
|||||
1 IAATGVPGTATVIRQYPKLLRAKANWEDTTFPSIEEKHRPRGSGVAGPVFRVNLGRAIP 60

Db

QY 532 SRAARAAEIH 541
|||||
61 SRAARAAEIH 70

Db

RESULT 15
US-09-450-072-77
; Sequence 77, Application US/09450072
; Patent No. 6358734
; GENERAL INFORMATION:
; APPLICANT: Delcayre, Alain
; TITLE OF INVENTION: Compounds for Treatment of Infectious and Immune System Disorders
; TITLE OF INVENTION: and Methods for their Use
; FILE REFERENCE: 11000.1042c1
; CURRENT APPLICATION NUMBER: US/09/450,072
; CURRENT FILING DATE: 1999-11-29
; EARLIER APPLICATION NUMBER: 09/351,348
; EARLIER FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 59
```

```
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-450-072-77

Query Match      11.4%; Score 326; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e-21;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 DQLGEPCAAQQRQGRGKHDRDRDVPAAQQRPAVHPAGPGPADRVGVDPGRHRRARQGHQPRD 281
|||||
1 DQLGEPCAAQQRQGRGKHDRDRDVPAAQQRPAVHPAGPGPADRVGVDPGRHRRARQGHQPRD 59

Db

Search completed: September 16, 2005, 20:36:26
Job time : 27 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2005, 20:36:34 ; Search time 168 Seconds
(without alignments)
1263.878 Million cell updates/sec

Title: US-10-607-752-116
Perfect score: 2862
Sequence: 1 IYSTFADRAYPGLTYSQHP.....IPSRARAAEINGSHHHHH 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum Match 100%
Listing first 45 summaries
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Match	Length	ID	Description
1	2862	100.0	582	AAB31660	Aab31660 Amino aci
2	2145	74.9	582	AAB31659	Aab31659 Amino aci
3	1906	66.6	582	AAB31658	Aab31658 Amino aci
4	490	17.1	97	AAB31650	Aab31650 Amino aci
5	440	15.4	87	AAB31653	Aab31653 Amino aci
6	389	13.6	75	AAB31649	Aab31649 Amino aci
7	373	13.0	70	AAB31648	Aab31648 Amino aci
8	326	11.4	59	AAB31656	Aab31656 Amino aci
9	255	8.9	49	AAB31651	Aab31651 Amino aci
10	237	8.3	46	AAB31652	Aab31652 Amino aci
11	224	7.8	44	AAB31655	Aab31655 Amino aci
12	222	7.8	456	AAB31655	Aab31655 Amino aci
13	220	7.7	445	AAB31655	Aab31655 Amino aci
14	206	7.2	38	AAB31646	Aab31646 Amino aci
15	204.5	7.1	819	AAB31646	Aab31646 Amino aci
16	197.5	6.9	900	AAB31646	Aab31646 Amino aci
17	196.5	6.9	606	AAB31646	Aab31646 Amino aci
18	196	6.8	613	AAB31646	Aab31646 Amino aci
19	194	6.8	973	AAB31646	Aab31646 Amino aci
20	192	6.7	802	AAB31646	Aab31646 Amino aci
21	191.5	6.7	672	AAB31646	Aab31646 Amino aci
22	190.5	6.7	1037	AAB31646	Aab31646 Amino aci
23	190.5	6.7	618	AAB31646	Aab31646 Amino aci
24	190.5	6.7	957	AAB31646	Aab31646 Amino aci
25	189.5	6.6	588	AAB31646	Aab31646 Amino aci

26	188.5	6.6	19938	6	ABP76678	Abp76678 Streptomy
27	186	6.5	726	7	ABO71929	AbO71929 Pseudomon
28	185	6.5	1246	7	ABO74394	AbO74394 Pseudomon
29	184.5	6.4	1139	4	AAU30127	AAU30127 Novel hum
30	183	6.4	19938	6	ABP76682	Abp76682 Streptomy
31	180.5	6.3	412	7	ABO74447	AbO74447 Pseudomon
32	180.5	6.3	822	7	ABO73733	AbO73733 Pseudomon
33	180.5	6.3	1706	7	ABO83014	AbO83014 Pseudomon
34	180	6.3	410	4	AAU79786	AAU79786 Coryneb
35	180	6.3	410	4	AAU79799	AAU79799 Coryneb
36	180	6.3	410	4	AAU79893	AAU79893 Coryneb
37	180	6.3	410	4	AAU79636	AAU79636 Coryneb
38	180	6.3	410	4	AAU71868	AAU71868 C. glutam
39	180	6.3	438	4	AAU92427	AAU92427 C. glutam
40	180	6.3	456	4	AAU79892	AAU79892 Coryneb
41	180	6.3	456	4	AAU79635	AAU79635 Coryneb
42	180	6.3	456	4	AAU79785	AAU79785 Coryneb
43	180	6.3	456	4	AAU79798	AAU79798 Coryneb
44	180	6.3	456	4	AAU71867	AAU71867 C. glutam
45	180	6.3	456	7	ADD13563	ADD13563 C. glutam

ALIGNMENTS

RESULT 1
AAB31660
ID AAB31660 standard; protein; 582 AA.

AC AAB31660;
DT 30-APR-2001 (first entry)
DE Amino acid sequence of an 8-mer multi-epitope designated ME/D.
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine.
OS Synthetic.
OS Mycobacterium vaccae.
XX WO200104140-A1.
XX 18-JAN-2001.
XX 10-JUL-2000; 2000WO-NZ000121.
XX 12-JUL-1999; 99US-00351348.
XX 29-NOV-1999; 99US-00450072.
XX (GENE-) GENESIS RES & DEV CORP. LTD.
XX Delcayre A;
XX WPI; 2001-168411/17.
XX N-PSDB; AAP25122.
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX vaccae, useful for treating mycobacterial infections, immune disorders
XX and cancers.
XX Claim 10; Page 75-76; 80pp; English.

App.

CC The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The...
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC represents an 8-mer multi-epitope designated ME/D
SQ Sequence 582 AA;

```
Query Match      100.0%; Score 2862; DB 4; Length 582;
Best Local Similarity 100.0%; Pred. No. 8e-215;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGRLDLAAR 60
DB 34 IYSTADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGRLDLAAR 93
QY 61 HRSVGEVRLGVLFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 120
DB 94 HRSVGEVRLGVLFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 153
QY 121 DGSISALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
DB 154 DGSISALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 213
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEFGAQQORQKH 240
DB 214 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEFGAQQORQKH 273
QY 241 RDVPAQQRPAPVHPAGPGPADRVGDPGRHRRARQHQPRDGSQASRTVSGVPVSNV 300
DB 274 RDVPAQQRPAPVHPAGPGPADRVGDPGRHRRARQHQPRDGSQASRTVSGVPVSNV 333
QY 301 LSAGIRCTPTTTRAVAIATLASRGVVAPOPAGDVVARAAAAGSPWVRSVARPVAVLRT 360
DB 334 LSAGIRCTPTTTRAVAIATLASRGVVAPOPAGDVVARAAAAGSPWVRSVARPVAVLRT 393
QY 361 GPPRRPSDTGSIQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 420
DB 394 GPPRRPSDTGSIQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGTVE 453
QY 421 IGSIALRCCKDEAVAAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 480
DB 454 IGSIALRCCKDEAVAAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGSIAATGPVPG 513
QY 481 TAWIVROYPKLURAKANWEDTWTTPSIEKHPRGSGVAGPVFRVNLGRAIPSAARAABEI 540
DB 514 TAWIVROYPKLURAKANWEDTWTTPSIEKHPRGSGVAGPVFRVNLGRAIPSAARAABEI 573
QY 541 HGSHHHHHH 549
DB 574 HGSHHHHHH 582

RESULT 2
AAB31659
ID AAB31659 standard; protein; 582 AA.
XX AAB31659;
AC AAB31659;
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of an 8-mer multi-epitope designated ME/B.
XX
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine.
XX
OS Synthetic.
OS Mycobacterium vaccae.
XX
FN WO200104140-A1.
XX
PD 18-JAN-2001.
XX
PF 10-JUL-2000; 2000WO-NZ000121.
XX
PR 12-JUL-1999; 99US-00351348.
XX 29-NOV-1999; 99US-00450072.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
```

```
PI Delcayre A;
XX WPI; 2001-168411/17.
DR N-PSDB; AAF25121.
XX
PT Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX
Claim 10; Page 74-75; 80pp; English.
XX
CC The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC represents an 8-mer multi-epitope designated ME/B
XX
SQ Sequence 582 AA;
Query Match      74.9%; Score 2145; DB 4; Length 582;
Best Local Similarity 67.4%; Pred. No. 8.7e-159;
Matches 442; Conservative 0; Mismatches 0; Indels 214; Gaps 4;

QY 1 IYSTADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGRLDLAAR 60
DB 34 IYSTADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQLVGLGRLDLAAR 93
QY 61 HRSVGEVRLGVLFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 120
DB 94 HRSVGEVRLGVLFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAGVGLGPGQRHARA 108
QY 121 DGSISALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 180
DB 109 -GSISSALVASPPRAASAPASIGLPGSQHTSIHPRSSNGSPVTHISQSMNAASSGTSR 167
QY 181 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGAGSDQLGEFGAQQORQKH 240
DB 168 RSSTLFRWQSPCMIPGSASSGLRESSQSASTCTDGNDSGA----- 207
QY 241 RDVPAQQRPAPVHPAGPGPADRVGDPGRHRRARQHQPRDGSQASRTVSGVPVSNV 300
DB 208 -----GSDRQASRTVSGVPVSNV 226
QY 301 LSAGIRCTPTTTRAVAIATLASRGVVAPOPAGDVVARAAAAGSPWVRSVARPVAVLRT 360
DB 227 LSAGIRCTPTTTRAVAIATLASRGVVAPOPAGDVVARAAAAGSPWVRSVARPVAVLRT 286
QY 361 GPPRRPSDT----- 370
DB 287 GPPRRPSDTGSDQLGEFGAQQORQKHRRDRDVPAAQRPAPVHPAGPGPADRVGDPGRH 346
QY 371 -----GSIQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGT 419
DB 347 RRARGHQPRDGSITQVGRPAVLFAPEQRCRRADQSCROIHPGGRHVQIVASARGT 406
QY 420 EIGSIARLCCKDEAVAAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALV----- 469
DB 407 EIGSIARLCCKDEAVAAALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALVGSDEPERAGL 466
QY 470 -----GSIATGVPVGTAWIVROYPKL 493
DB 467 VEVLGAQCRDRDVGAGDAAGVGLGPGQRHRRADGSIATGVPVGTAWIVROYPKL 526
QY 494 AKANWEDTWTTPSIEKHPRGSGVAGPVFRVNLGRAIPSAARAABEIHGSHHHHHH 549
DB 527 AKANWEDTWTTPSIEKHPRGSGVAGPVFRVNLGRAIPSAARAABEIHGSHHHHHH 582

RESULT 3
AAB31658
```

```

ID  AAB31658 standard; protein; 582 AA.
XX  AC
XX  AAB31658;
XX  DT
XX  30-APR-2001 (first entry)
XX  DE
XX  Amino acid sequence of an 8-mer multi-epitope designated ME/A.
XX  Epitope; antigen; cytokine production; immune disorder; tuberculosis;
XX  KW cancer; mycobacterial infection; TH1 immune response; vaccine.
XX  OS
XX  OS Mycobacterium vaccae.
XX  WO200104140-A1.
XX  PN
XX  PD
XX  PD
XX  PD
XX  PF
XX  PF 10-JUL-2000; 2000WO-NZ000121.
XX  XX
XX  PR 12-JUL-1999; 99US-00351348.
XX  PR 29-NOV-1999; 99US-00450072.
XX  (GENE-) GENESIS RES & DEV CORP LTD.
XX  Delcayre A;
XX  WPI; 2001-168411/17.
XX  DR N-PSDB; AAF25120.
XX  Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX  Claim 10; Page 73-74; 80pp; English.
XX  The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC represents an 8-mer multi-epitope designated ME/A
XX  Sequence 582 AA;
XX  Query Match 66.6%; Score 1906; DB 4; Length 582;
XX  Best Local Similarity 57.1%; Pred. No. 4.1e-140;
XX  Matches 399; Conservative 0; Mismatches 0; Indels 300; Gaps 2;
XX  1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDGVMNAARIGEOVLGRLDLAAR 60
XX  34 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDGVMNAARIGEOVLGRLDLAAR 93
XX  61 HRSVGEVRLGLVFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAGVGLGPORHARA 120
XX  94 HRSVGEVRLGLVFWAGSDPERAGLVEVLGAQCRDRDVGAGDAAGVGLGPORHARA 153
XX  121 ----- 120
XX  154 DGSQRQASRTSGVPVSNVLSAGIRCRTPTTTRAVAICLATLASRGVAPAGDVARAA 213
XX  121 ----- 120
XX  214 AAGSPWVRSVARPVAVLRTGPPRRPDSGTGDLGEPGAQQRQKHKRDREDVPAQQR 273
XX  121 ----- DGSISALVASPPRAASAPASIGLPGSGQ 150
XX  274 AVHPAGPGPADRVGDPGRHRRARQHQHQRDGSISALVASPPRAASAPASIGLPGSGQ 333
XX  151 HTSIHPRSSNGSPPTVHISQSMNAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSAS 210

```

```

Db 334 HTSIHPRSSNGSPPTVHISQSMNAASGTSRRSSTLFRWQSPCMIPGSASSGLRESSQSAS 393
Qy 211 TCTDGNDSGAGSDQLGEPGAQQRQKHKRDREDVPAQQRPAVHPAGPGPADRVGDPGRH 270
Db 394 TCTDGNDSGA----- 403
Qy 271 RRAQGHQHPDRGSDRQASRTVSGVPVSNVLSAGIRCRTPTTTRAVAICLATLASRGVAP 330
Db 404 ----- 403
Qy 331 QPAGDVARAAGASPPWVRSVARPVAVLRTGPPRRPDSGTGDLGEPGAQQRQKHKRDREDV 390
Db 404 -----GSITQVGRPAVLFAPEQR 423
Qy 391 RRAQGHQHPDRGSDRQASRTVSGVPVSNVLSAGIRCRTPTTTRAVAICLATLASRGVAP 450
Db 424 RRAQGHQHPDRGSDRQASRTVSGVPVSNVLSAGIRCRTPTTTRAVAICLATLASRGVAP 483
Qy 451 DRALNIGPYLPAEVPALVGSIAATGPVPGTAWIVRQYPKLLRAKANWEDTWTFFSIEBK 510
Db 484 DRALNIGPYLPAEVPALVGSIAATGPVPGTAWIVRQYPKLLRAKANWEDTWTFFSIEBK 543
Qy 511 HRPRGSVAGPVFRVNLGRAIPSRARAEEIHGSHHHHHH 549
Db 544 HRPRGSVAGPVFRVNLGRAIPSRARAEEIHGSHHHHHH 582

```

RESULT 4

AAB31650

ID AAB31650 standard; peptide; 97 AA.

XX AAB31650;

XX 30-APR-2001 (first entry)

DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA26.

Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 cancer; mycobacterial infection; TH1 immune response; vaccine.

OS Mycobacterium vaccae.

PN WO200104140-A1.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-NZ000121.

XX 12-JUL-1999; 99US-00351348.

XX 29-NOV-1999; 99US-00450072.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;

XX WPI; 2001-168411/17.

XX N-PSDB; AAF25081.

Novel polypeptides comprising immunogenic epitopes of Mycobacterium
 vaccae, useful for treating mycobacterial infections, immune disorders
 and cancers.

PS Claim 1; Page 70-71; 80pp; English.

The specification describes an immunogenic epitope of a Mycobacterium
 vaccae antigen. The epitope is a stimulator of cytokine production. The
 epitopes are useful for the treatment of immune disorders, infectious
 diseases, especially tuberculosis, and cancer. They are also useful for
 treatment of other mycobacterial infections such as those caused by
 Mycobacterium avium. The epitopes are especially useful for inducing TH1
 immune responses, and for producing vaccines. The present sequence
 represents a M. vaccae epitope of the invention

XX

```
SQ Sequence 97 AA;
  Query Match      17.1%; Score 490; DB 4; Length 97;
  Best Local Similarity 100.0%; Pred. No. 1.8e-30;
  Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 ISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNNAASSGTSRRSS 183
Db 1 ISSALVASPPRAASAPASIGLPGSGQHTSIHPRSSNGSPVTHISQSNNAASSGTSRRSS 60

QY 184 TLFRRQSPCMIPGSASSGLRESSQSASTCTDGNDSGA 220
Db 61 TLFRRQSPCMIPGSASSGLRESSQSASTCTDGNDSGA 97

RESULT 5
331653
AAB31653 standard; peptide; 87 AA.
AC AAB31653;
DT 30-APR-2001 (first entry)
DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA37.
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine.
OS Mycobacterium vaccae.
XX WO200104140-A1.
XX 18-JAN-2001.
XX 10-JUL-2000; 2000WO-NZ000121.
XX 12-JUL-1999; 99US-00351348.
XX 29-NOV-1999; 99US-00450072.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Delcayre A;
XX WPI; 2001-168411/17.
XX N-PSDB; AAF25084.
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX Claim 1; Page 71; 80pp; English.
XX The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC represents a M. vaccae epitope of the invention
XX Sequence 87 AA;
  Query Match      15.4%; Score 440; DB 4; Length 87;
  Best Local Similarity 100.0%; Pred. No. 1.3e-26;
  Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 284 DRQASRTVSGVPVESNVLSSAGIRCTPTTTRAVAIATLASRGVAPQAGDVARAAAG 343
Db 1 DRQASRTVSGVPVESNVLSSAGIRCTPTTTRAVAIATLASRGVAPQAGDVARAAAG 60

QY 344 SPMPVRSVARPVAVLRTGPPRRPSDT 370
  |||||||
```

```
Db 61 SPMPVRSVARPVAVLRTGPPRRPSDT 87

RESULT 6
AAB31649
ID AAB31649 standard; peptide; 75 AA.
XX AAB31649;
AC AAB31649;
DT 30-APR-2001 (first entry)
DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA9A.
KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
KW cancer; mycobacterial infection; TH1 immune response; vaccine.
OS Mycobacterium vaccae.
XX WO200104140-A1.
XX 18-JAN-2001.
XX 10-JUL-2000; 2000WO-NZ000121.
XX 12-JUL-1999; 99US-00351348.
XX 29-NOV-1999; 99US-00450072.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Delcayre A;
XX WPI; 2001-168411/17.
XX N-PSDB; AAF25080.
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX Claim 1; Page 70; 80pp; English.
XX The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC represents a M. vaccae epitope of the invention
XX Sequence 75 AA;
  Query Match      13.6%; Score 389; DB 4; Length 75;
  Best Local Similarity 100.0%; Pred. No. 1e-22;
  Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQVLGPGRLDLAAR 60
Db 1 IYSTFADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQVLGPGRLDLAAR 60

QY 61 HRSVGEVRLGLGVFWA 75
Db 61 HRSVGEVRLGLGVFWA 75

RESULT 7
AAB31648
ID AAB31648 standard; peptide; 70 AA.
XX AAB31648;
AC AAB31648;
DT 30-APR-2001 (first entry)
DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA5.
```

```

XX KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
XX KW cancer; mycobacterial infection; TH1 immune response; vaccine.
XX OS Mycobacterium vaccae.
XX PN WO200104140-A1.
XX PD 18-JAN-2001.
XX PF 10-JUL-2000; 2000WO-NZ000121.
XX PR 12-JUL-1999; 99US-00351348.
XX PR 29-NOV-1999; 99US-00450072.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Delcayre A;
XX PR WPI; 2001-168411/17.
XX DR N-PSDB; AAF25079.
XX CC Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX CC vaccae, useful for treating mycobacterial infections, immune disorders
XX PT and cancers.
XX PS Claim 1; Page 70; 80pp; English.
XX CC The specification describes an immunogenic epitope of a Mycobacterium
XX CC vaccae antigen. The epitope is a stimulator of cytokine production. The
XX CC epitopes are useful for the treatment of immune disorders, infectious
XX CC diseases, especially tuberculosis, and cancer. They are also useful for
XX CC treatment of other mycobacterial infections such as those caused by
XX CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX CC immune responses, and for producing vaccines. The present sequence
XX CC represents a M. vaccae epitope of the invention
XX SQ Sequence 70 AA;
XX Query Match 13.0%; Score 373; DB 4; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-21;
XX Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 472 IAATGVPCTAIVRQYKLLRAKANWEDTTFPSIEEKHRPGSVAGVFRVNLGRAIP 531
XX Db 1 IAATGVPCTAIVRQYKLLRAKANWEDTTFPSIEEKHRPGSVAGVFRVNLGRAIP 60
XX
XX QY 532 SRAARAAEIH 541
XX Db 61 SRAARAAEIH 70
XX
XX RESULT 8
XX AAB31656
XX ID AAB31656 standard; peptide; 59 AA.
XX AC AAB31656;
XX DT 30-APR-2001 (first entry)
XX DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA45.
XX KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
XX KW cancer; mycobacterial infection; TH1 immune response; vaccine.
XX OS Mycobacterium vaccae.
XX PN WO200104140-A1.
XX PD 18-JAN-2001.
XX PF 10-JUL-2000; 2000WO-NZ000121.
XX PR 12-JUL-1999; 99US-00351348.
XX PR 29-NOV-1999; 99US-00450072.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Delcayre A;
XX PR WPI; 2001-168411/17.
XX DR N-PSDB; AAF25082.
XX CC Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX CC vaccae, useful for treating mycobacterial infections, immune disorders
XX PT and cancers.
XX PS Claim 1; Page 71; 80pp; English.
XX CC The specification describes an immunogenic epitope of a Mycobacterium
XX CC vaccae antigen. The epitope is a stimulator of cytokine production. The
XX CC epitopes are useful for the treatment of immune disorders, infectious
XX CC diseases, especially tuberculosis, and cancer. They are also useful for
XX CC treatment of other mycobacterial infections such as those caused by
XX CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX CC immune responses, and for producing vaccines. The present sequence
XX CC represents a M. vaccae epitope of the invention
XX SQ Sequence 59 AA;
XX Query Match 11.4%; Score 326; DB 4; Length 59;
XX Best Local Similarity 100.0%; Pred. No. 6.2e-18;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 223 DOLGSPGAQQQRGKRRDRDVPAAQORPAVHPAGPGPADRVGVDPGRHRRARGQHPRD 281
XX Db 1 DOLGSPGAQQQRGKRRDRDVPAAQORPAVHPAGPGPADRVGVDPGRHRRARGQHPRD 59
XX
XX RESULT 9
XX AAB31651
XX ID AAB31651 standard; peptide; 49 AA.
XX AC AAB31651;
XX DT 30-APR-2001 (first entry)
XX DE Amino acid sequence of a M. vaccae immunogenic epitope from DNA27.
XX KW Epitope; antigen; cytokine production; immune disorder; tuberculosis;
XX KW cancer; mycobacterial infection; TH1 immune response; vaccine.
XX OS Mycobacterium vaccae.
XX PN WO200104140-A1.
XX PD 18-JAN-2001.
XX PF 10-JUL-2000; 2000WO-NZ000121.
XX PR 12-JUL-1999; 99US-00351348.
XX PR 29-NOV-1999; 99US-00450072.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX PI Delcayre A;
XX PR WPI; 2001-168411/17.
XX DR N-PSDB; AAF25082.
XX CC Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX CC vaccae, useful for treating mycobacterial infections, immune disorders
XX PT and cancers.
XX PS Claim 1; Page 71; 80pp; English.
XX CC The specification describes an immunogenic epitope of a Mycobacterium
XX CC vaccae antigen. The epitope is a stimulator of cytokine production. The
XX CC epitopes are useful for the treatment of immune disorders, infectious
XX CC diseases, especially tuberculosis, and cancer. They are also useful for
XX CC treatment of other mycobacterial infections such as those caused by
XX CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX CC immune responses, and for producing vaccines. The present sequence
XX CC represents a M. vaccae epitope of the invention
XX SQ Sequence 59 AA;
XX Query Match 11.4%; Score 326; DB 4; Length 59;
XX Best Local Similarity 100.0%; Pred. No. 6.2e-18;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 223 DOLGSPGAQQQRGKRRDRDVPAAQORPAVHPAGPGPADRVGVDPGRHRRARGQHPRD 281
XX Db 1 DOLGSPGAQQQRGKRRDRDVPAAQORPAVHPAGPGPADRVGVDPGRHRRARGQHPRD 59
XX

```

CC The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC represents a M. vaccae epitope of the invention
XX
SQ Sequence 49 AA;

Query Match 8.9%; Score 255; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.7e-12; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0;

QY 373 ITQVGRPAVLFAPEQRCRRRQDSRCQTHPGGGRHVQIVASARGTVEI 421
1 ITQVGRPAVLFAPEQRCRRRQDSRCQTHPGGGRHVQIVASARGTVEI 49

RESULT 10
AAB31652
ID AAB31652 standard; peptide; 46 AA.

AC AAB31652;

XX 30-APR-2001 (first entry)

XX Amino acid sequence of a M. vaccae immunogenic epitope from DNA29.

XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
XX cancer; mycobacterial infection; TH1 immune response; vaccine.

XX Mycobacterium vaccae.

XX WO200104140-A1.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-NZ000121.

XX 12-JUL-1999; 99US-00351348.

XX 29-NOV-1999; 99US-00450072.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;

XX WPI; 2001-168411/17.

XX N-PSDB; AAF25083.

XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX vaccae, useful for treating mycobacterial infections, immune disorders
XX and cancers.

XX Claim 1; Page 71; 80pp; English.

XX The specification describes an immunogenic epitope of a Mycobacterium
XX vaccae antigen. The epitope is a stimulator of cytokine production. The
XX epitopes are useful for the treatment of immune disorders, infectious
XX diseases, especially tuberculosis, and cancer. They are also useful for
XX treatment of other mycobacterial infections such as those caused by
XX Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX immune responses, and for producing vaccines. The present sequence
XX represents a M. vaccae epitope of the invention
XX

SQ Sequence 46 AA;

Query Match 8.3%; Score 237; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.1e-11; Indels 0; Gaps 0;
Matches 46; Conservative 0; Mismatches 0;

QY 424 IARLCGKDEAVALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALV 469

Db 1 IARLCGKDEAVALHYVAPVGEKQDYIDRALRNIGPYLPAEVPALV 46

RESULT 11

AAB31655

ID AAB31655 standard; peptide; 44 AA.

AC AAB31655;

XX 30-APR-2001 (first entry)

XX Amino acid sequence of a M. vaccae immunogenic epitope from DNA44.

XX Epitope; antigen; cytokine production; immune disorder; tuberculosis;
XX cancer; mycobacterial infection; TH1 immune response; vaccine.

XX Mycobacterium vaccae.

XX WO200104140-A1.

XX 18-JAN-2001.

XX 10-JUL-2000; 2000WO-NZ000121.

XX 12-JUL-1999; 99US-00351348.

XX 29-NOV-1999; 99US-00450072.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Delcayre A;

XX WPI; 2001-168411/17.

XX N-PSDB; AAF25086.

XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
XX vaccae, useful for treating mycobacterial infections, immune disorders
XX and cancers.

XX Claim 1; Page 72; 80pp; English.

XX The specification describes an immunogenic epitope of a Mycobacterium
XX vaccae antigen. The epitope is a stimulator of cytokine production. The
XX epitopes are useful for the treatment of immune disorders, infectious
XX diseases, especially tuberculosis, and cancer. They are also useful for
XX treatment of other mycobacterial infections such as those caused by
XX Mycobacterium avium. The epitopes are especially useful for inducing TH1
XX immune responses, and for producing vaccines. The present sequence
XX represents a M. vaccae epitope of the invention
XX

SQ Sequence 44 AA;

Query Match 7.8%; Score 224; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 4e-10; Indels 0; Gaps 0;
Matches 44; Conservative 0; Mismatches 0;

QY 78 DPERAGLRVEVLGACRRRDVVAGDAAAVGLGFGQRHARAD 121

Db 1 DPERAGLRVEVLGACRRRDVVAGDAAAVGLGFGQRHARAD 44

RESULT 12

ABO66648

ID ABO66648 standard; protein; 456 AA.

AC ABO66648;

XX 29-JUL-2004 (first entry)

XX Klebsiella pneumoniae polypeptide seqid 13165.

XX Recombinant expression vector; transcription regulatory element;
XX Klebsiella pneumoniae protein; antibacterial; Vaccine.

XX Klebsiella pneumoniae.
 OS US6610836-B1.
 XX 26-AUG-2003.
 XX 27-JAN-2000; 2000US-00489039.
 XX 29-JAN-1999; 99US-0117747P.
 XX (GENO-) GENOME THERAPEUTICS CORP.
 XX Breton GL, Osborne M;
 PI WPI; 2003-895346/82.
 DR N-PSDB; ABD00219.
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 XX Disclosure; SEQ ID NO 13165; 932pp; English.
 PS The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX Sequence 456 AA;
 SQ Query Match 7.8%; Score 222; DB 7; Length 456;
 Best Local Similarity 46.2%; Pred. No. 1.2e-08;
 Matches 49; Conservative 17; Mismatches 30; Indels 10; Gaps 1;
 QY 5 FADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQVLGPGRLDLAARHSV 64
 DB 315 FDDHFFAGGLTYSGHPLAWAIVATIDAMKEENVVNAASIGNEVLRPGLEALAEKHAI 374
 QY 65 GEVRGLGVFWAGSDPERAGLVEVLGAQCRRRDVVVGAGDAAAVGV 110
 DB 375 GEVRGRLGFOA-----LELVSSREQKTPLTAAADMAAIGKAL 410
 RESULT 13
 AAU36108
 ID AAU36108 standard; protein; 445 AA.
 XX AAU36108;
 DT 14-FEB-2002 (first entry)
 XX Klebsiella pneumoniae cellular proliferation protein #96.
 XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 XX Klebsiella pneumoniae.
 OS WO200170955-A2.
 XX 27-SEP-2001.
 XX 21-MAR-2001; 2001WO-US009180.
 XX 21-MAR-2000; 2000US-0191078P.
 XX 23-MAY-2000; 2000US-0208848P.
 XX 26-MAY-2000; 2000US-0207727P.
 XX 23-OCT-2000; 2000US-0242578P.
 XX 27-NOV-2000; 2000US-0253625P.
 XX 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS53967.
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX Example 3; SEQ ID NO 11701; 511pp; English.
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 445 AA;
 SQ Query Match 7.7%; Score 220; DB 4; Length 445;
 Best Local Similarity 46.2%; Pred. No. 1.7e-08;
 Matches 49; Conservative 17; Mismatches 30; Indels 10; Gaps 1;
 QY 5 FADRAYPGGLTYSGHPLATACAVATINAMEDEGMVANAARIGEQVLGPGRLDLAARHSV 64
 DB 304 FDDHFFAGGLTYSGHPLAWAIVATIDAMKEEKVVENAASIGNEVLRPGLEALAEKHAI 363
 QY 65 GEVRGLGVFWAGSDPERAGLVEVLGAQCRRRDVVVGAGDAAAVGV 110
 DB 364 GEVRGRLGFOA-----LELVSSREQKTPLTAAADMAAIGKAL 399
 RESULT 14
 AAB31646
 ID AAB31646 standard; peptide; 38 AA.
 XX AAB31646;
 AC AAB31646;
 XX 30-APR-2001 (first entry)
 XX Amino acid sequence of a M. vaccae immunogenic epitope from DNA27.
 DE Epitope; antigen; cytokine production; immune disorder; tuberculosis;
 KW cancer; mycobacterial infection; TH1 immune response; vaccine.
 XX Mycobacterium vaccae.
 OS WO200104140-A1.
 XX 18-JAN-2001.
 XX 10-JUL-2000; 2000WO-NZ000121.
 XX 12-JUL-1999; 99US-00351348.
 XX 29-NOV-1999; 99US-00450072.

```
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX Delcayre A;
XX WPI; 2001-168411/17.
XX DR N-PSDB; AAF25077.
XX Novel polypeptides comprising immunogenic epitopes of Mycobacterium
PT vaccae, useful for treating mycobacterial infections, immune disorders
PT and cancers.
XX Claim 1; Page 70; 80pp; English.
XX The specification describes an immunogenic epitope of a Mycobacterium
CC vaccae antigen. The epitope is a stimulator of cytokine production. The
CC epitopes are useful for the treatment of immune disorders, infectious
CC diseases, especially tuberculosis, and cancer. They are also useful for
CC treatment of other mycobacterial infections such as those caused by
CC Mycobacterium avium. The epitopes are especially useful for inducing TH1
CC immune responses, and for producing vaccines. The present sequence
CC represents a M. vaccae epitope of the invention
XX Sequence 38 AA;
XX
XX Query Match 7.2%; Score 206; DB 4; Length 38;
XX Best Local Similarity 100.0%; Pred. No. 8.4e-09; Mismatches 0; Indels 0; Gaps 0;
XX Matches 38; Conservative 0;
XX
XX QY 373 ITQGRPAVLFAPEQRCRRRDRQSCRQIHFGGGRHVQ 410
XX |||||
XX DB 1 ITQGRPAVLFAPEQRCRRRDRQSCRQIHFGGGRHVQ 38
XX
XX RESULT 15
XX ABO70823
XX ID ABO70823 standard; protein; 819 AA.
XX AC ABO70823;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Pseudomonas aeruginosa polypeptide #2998.
XX
XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX Pseudomonas aeruginosa.
XX
XX PN US6551795-B1.
XX
XX PD 22-APR-2003.
XX
XX PF 18-FEB-1999; 99US-00252991.
XX
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX WPI; 2003-615309/58.
XX DR N-PSDB; ABD04394.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX PS Disclosure; SEQ ID NO 19569; 455pp; English.
XX
XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
```

```
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
XX Sequence 819 AA;
XX
XX Query Match 7.1%; Score 204.5; DB 7; Length 819;
XX Best Local Similarity 25.5%; Pred. No. 6.1e-07;
XX Matches 161; Conservative 53; Mismatches 241; Indels 177; Gaps 34;
XX
XX QY 9 AYPG--GLTYSGHPLATACAVATTNAMEDEGMVANAARIGEOVLGPGLRDLAARRHSVGE 66
XX |||||
XX DB 202 AFGNVGALVRGCDGHARAAAVMHGOQPGGLASRSVGAG----GSGQRDPAGDPG-DQ 256
XX
XX QY 67 VRGLGVFWAGSDPERAGLRVEVLGACQCRRRDVVGAGDAAAVGVVLGPQR-OHRA----- 118
XX |||||
XX DB 257 LRG-----PPAPALRLHL-----RAPAAAGRRHQHQRVRRADLPEHL 295
XX
XX QY 119 ---RAD--GSISSALVASPPRAASAPASIGLGPS-----GQHTSIHPRSSNGSPVTHI 167
XX |||||
XX DB 296 FHRADRPVRVPRVPAAFRAAAVPAAD-GLDPHSRLPGLGDHGAQPPRAASG----- 348
XX
XX QY 168 SQSMAAASSGTSRRSSSTLFRWQSPCMIPGSSGLRESSQSASTC--TDGNDSGAGSDQL 225
XX |||||
XX DB 349 ---CHRRGAVPRRHGILGDRHGPVAGGAAGVQGRGAVDPARLFRRTPGRAVVPGDHLC 404
XX
XX QY 226 GEPGAQQRQKGRDRDVPQAQRPVHPAGPG-PADRVGVDPGRHRRARQHOHPRDGS 284
XX |||||
XX DB 405 GRPGTGPRPGAR-----PARRAYQLLPDGEALPA-----PGR-RNLLGAHQEVAGAR 450
XX
XX QY 285 ROASRTV-----SGVVFESNVLISAGIRC--RT-----PTTRAVAIICLATL 322
XX |||||
XX DB 451 RGSRPVLRHPGCGYRQSQACRAGARPRRTDQAGHRRRDRHLGVGPGAPPALGFPHV 510
XX
XX QY 323 A-----SRGVVAPQA--GDVARAAAGSPWVRVSVARVPVAVLRGPPRRPSD 369
XX |||||
XX DB 511 RVRHPQRSRRRGAVEGEPACGRSPRAARAGAR-----RORVAEIRLVPRVPQP 564
XX
XX QY 370 TGSITQVGRPAVLFAPEQRCRR-----RADQRCRQIHFGGGRHVQI1VASARGTVEI 421
XX |||||
XX DB 565 RGSPPAGDRHA-----DAERGQPSGADDRHQRRHDDPHPGN-----PARGKGTAG 612
XX
XX QY 422 GSI-ARLCGKD---EAVAALHYVAPVGEKQYIDRALRN----- 456
XX |||||
XX DB 613 DPFVHRRCRVDHRRRRPRDLH--BPGGGRDRLDLAGHRRRAPRTGLQARQRHRRGPGK 670
XX
XX QY 457 IGPVLPAREVPALV--GSTAATGPVPGTAWIVROYPKLLRAKAN--WEDTWTFFPSTEEXHR 512
XX |||||
XX DB 671 PGATLPAEHGVLPGGRRHADQPOGRAA----RIPELRCAGAHPRWRDHRHRAVGPERHQ 726
XX
XX QY 513 PRGSVAGFVRVNLGR--AIFPSRAARAABEIHG 542
XX |||||
XX DB 727 GPGDAA----RAELSRLPRCPHRAVQPHQVRG 754
XX
```

Search completed: September 16, 2005, 20:55:01
Job time : 171 secs